

```

RESULT 8
Q8UVX5 PRELIMINARY; PRT; 127 AA.
AC Q8UVX5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Onconase precursor.
GN RPR.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN 1
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Wang S.-C.;
RT "Rana pipiens onconase genomic DNA.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332139; AAL54383.1; -
DR PIR; A39035; A39035.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea.1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
SQ SEQUENCE 127 AA; 14469 MW; 953F9D351CFEEF3 CRC64;

Query Match 45.6%; Score 273.5; DB 13; Length 127;
Best Local Similarity 48.6%; Pred. No. 1.2e-23;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVI-NLN 58
Db 24 QDWLTFQKHITTDTRVDVDCNLMPTSLF---HCKDKNTFIYSRPEPVKAICKGIIASKN 79

QY 59 VLSSTFQMLNCTRTSITPR-PCPYSSRTETNYICVKCENQYVHFAGIGRC 109
Db 80 VLITSEFYSDC---NVTSRCKYKLNKSTNKFCTCENQAPVHFVGVGSC 127

RESULT 9
Q9DFY6 PRELIMINARY; PRT; 129 AA.
AC Q9DFY6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RC-RNase4 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN 1
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN 2
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242553; AAG31439.1; -
DR PDB; 1M58; 09-JAN-03.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea.1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNASE2 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14839 MW; 989719CF52053ECC CRC64;

Query Match 37.6%; Score 225.5; DB 13; Length 128;
Best Local Similarity 39.3%; Pred. No. 4.1e-18;
Matches 44; Conservative 21; Mismatches 38; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVI-NLN 58
Db 24 QNWETFQKHITDTRVDVDCNLMPTSLF---DCKDKNTFIYARPGRVQALCKNIIVSKN 79

QY 59 VLSSTFQMLNCTRTSITPR-PCPYSSRTETNYICVKCENQYVHFAGIGRC 110
Db 80 VLSTDEFYLSDCNRIKL---PCHYKLNKSSNTICITCENKLPVHFVAVEECP 128

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DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea.1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 129 RC-RNASE4 RIBONUCLEASE.
SQ SEQUENCE 129 AA; 14724 MW; 826A62882B10ABDA CRC64;

Query Match 40.5%; Score 243; DB 13; Length 129;
Best Local Similarity 42.5%; Pred. No. 4e-20;
Matches 48; Conservative 25; Mismatches 30; Indels 10; Gaps 5;

QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVI-NLN 58
Db 24 QDWATFKKHLTDTVDVDCNLMPTSLF---DCKDKNTFIYSLPGPVKALCRGVIFSAD 79

QY 59 VLSSTFQMLNCTRTSITPR-PCPYSSRTETNYICVKCENQYVHFAGIGRC 110
Db 80 VLSNSEFYLAEC---NVKPRKPKCYKLNKSSNRICIRCEHELFVHFAGVGICP 129

RESULT 10
Q9DFY8 PRELIMINARY; PRT; 128 AA.
AC Q9DFY8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RC-RNase2 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN 1
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN 2
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242553; AAG31439.1; -
DR PDB; 1M58; 09-JAN-03.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea.1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNASE2 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14839 MW; 989719CF52053ECC CRC64;

Query Match 37.6%; Score 225.5; DB 13; Length 128;
Best Local Similarity 39.3%; Pred. No. 4.1e-18;
Matches 44; Conservative 21; Mismatches 38; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVI-NLN 58
Db 24 QNWETFQKHITDTRVDVDCNLMPTSLF---DCKDKNTFIYARPGRVQALCKNIIVSKN 79

QY 59 VLSSTFQMLNCTRTSITPR-PCPYSSRTETNYICVKCENQYVHFAGIGRC 110
Db 80 VLSTDEFYLSDCNRIKL---PCHYKLNKSSNTICITCENKLPVHFVAVEECP 128

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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:10 ; Search time 31.2816 Seconds  
(without alignments)  
1109.503 Million cell updates/sec

Title: US-09-961-400-19

Perfect score: 600

Sequence: 1 QNWATPQQKHINTPIICNT.....ICVKCENQYVHFAGIGRCP 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phase:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_rvirus:\*

16: sp\_bacteriap:\*

17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	554.5	92.4	133	13	Q98SM0 rana catesb
2	483.5	80.6	132	13	Q98SM2 rana catesb
3	474.5	79.1	133	13	Q98SL9 rana catesb
4	467.5	77.9	133	13	Q98SL8 rana catesb
5	444.5	74.1	132	13	Q98SM1 rana catesb
6	372	62.0	132	13	Q9DF78 rana catesb
7	277.5	46.2	127	13	Q918V8 rana pipien
8	273.5	45.6	127	13	Q8UVX5 rana pipien
9	243	40.5	129	13	Q9DFY6 rana pipien
10	225.5	37.6	128	13	Q9DFY8 rana catesb
11	223.5	37.2	128	13	Q9DFY7 rana catesb
12	214.5	35.8	128	13	Q9DFY5 rana catesb
13	161	26.8	169	13	Q9W738 xenopus lae
14	128	21.3	170	6	Q9BEC1 rana pipien
15	127.5	21.2	144	11	Q80Z85 mus musculus
16	127.5	21.2	153	11	Q80XS4 mus musculus

17	123.5	20.6	147	6	Q7YRJ6	Q7YRJ6 balaena mys
18	122	20.3	146	6	Q861Y5	Q861Y5 colobus gue
19	121.5	20.2	116	6	Q9TVC0	Q9TVC0 sus scrofa
20	121.5	20.2	163	6	Q9BDC2	Q9BDC2 antilocapra
21	121	20.2	150	11	Q8VD94	Q8VD94 berylmys bo
22	119	19.8	150	11	Q8VD88	Q8VD88 rattus norv
23	118.5	19.8	144	6	Q9BH14	Q9BH14 antilocapra
24	118.5	19.8	147	6	Q7YRJ5	Q7YRJ5 tursiops tr
25	116.5	19.4	149	11	Q8K2T2	Q8K2T2 mus musculus
26	116.5	19.4	149	11	Q8C6G3	Q8C6G3 mus musculus
27	116	19.3	146	6	Q861Y4	Q861Y4 trachypithe
28	116	19.3	150	11	Q8VD92	Q8VD92 rattus exul
29	115	19.2	146	6	Q861Y3	Q861Y3 pygathrix r
30	115	19.2	146	6	Q861Y2	Q861Y2 pygathrix b
31	115	19.2	146	6	Q861Y1	Q861Y1 pygathrix a
32	113.5	18.9	152	11	Q8VD89	Q8VD89 rattus norv
33	111	18.5	148	11	Q8C6G3	Q8C6G3 mus musculus
34	110.5	18.4	124	6	Q95NE6	Q95NE6 bubalus bub
35	109.5	18.2	148	11	Q8C7E4	Q8C7E4 mus musculus
36	109.5	18.2	149	11	Q8VD95	Q8VD95 berylmys bo
37	109	18.2	124	6	Q9BEC2	Q9BEC2 tragulus ja
38	109	18.2	134	6	Q9BDB9	Q9BDB9 tragulus ja
39	108.5	18.1	152	11	Q8VD84	Q8VD84 rattus tiom
40	108.5	18.1	156	6	Q8SQ05	Q8SQ05 lagotherax l
41	107.5	17.9	119	6	Q9TV28	Q9TV28 eulemur ful
42	107.5	17.9	119	6	Q9TV30	Q9TV30 saguinus oe
43	106.5	17.8	156	6	Q8SQ06	Q8SQ06 ateles geof
44	105.5	17.6	142	6	Q9BEC3	Q9BEC3 tragulus ja
45	105.5	17.6	156	6	Q8SQ08	Q8SQ08 saimiri sci

## ALIGNMENTS

### RESULT 1

Q98SM0	PRELIMINARY;	PRT;	133 AA.
ID	Q98SM0		
AC	Q98SM0;		
DT	01-JUN-2001 (TREMblrel. 17, Created)		
DT	01-JUN-2001 (TREMblrel. 17, Last sequence update)		
DT	01-OCT-2003 (TREMblrel. 25, Last annotation update)		
DE	RNase A-type ribonuclease rc208 precursor.		
OS	Rana catesbeiana (Bull frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.		
OX	NCBI_TaxID=8400;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21539506; PubMed=11683320;		
RA	Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;		
RT	"Rapid diversification of RNase A superfamily ribonuclease from the		
RT	bullfrog, Rana catesbeiana.";		
RL	J. Mol. Evol. 53:31-38(2001).		
DR	EMBL; AF351209; AAK30255.1; -		
DR	HSSP; P11916; 1BC4.		
DR	GO; GO:0003676; F:nucleic acid binding; IEA.		
DR	GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.		
DR	InterPro; IPR001427; RNaseA.		
DR	Pfam; PF000074; rnasea; 1.		
DR	ProDom; PD000535; RNaseA; 1.		
DR	SMART; SM00092; RNase_Pc; 1.		
DR	PROSITE; PS00127; RNASE_PANGREATIC; 1.		
XM	Signal.		
FT	SIGNAL		
SQ	SEQUENCE	133 AA; 14628 MW; 87FCF122C3499E02 CRC64;	

Query Match	92.4%;	Score 554.5;	DB 13;	Length 133;
Best Local Similarity	92.8%;	Pred. No. 5.6e-56;		
Matches 103;	Conservative	2;	Mismatches	5;
			Indels	1;
			Gaps	1;
QY	1	QNWATPQQKHINTPII-CNTILDNNIYVGGCKRVNTFIISATTVKAICTGVINLV	59	
Db	23	QNWATPQQKHINTPII-CNTILDNNIYVGGCKRVNTFIISATTVKAICTGVINLV	82	



ID	Q9BEC1	PRELIMINARY;	PRT;	170 AA.
AC	Q9BEC1;			
AC	Q9BEC1;			
DT	01-JUN-2001	(TREMELrel. 17, Created)		
DT	01-JUN-2001	(TREMELrel. 17, Last sequence update)		
DT	01-JUN-2003	(TREMELrel. 24, Last annotation update)		
DE		Brain-type ribonuclease ribonuclease precursor (fragment).		
DE		RNAse B.		
GN		Tragulus javanicus (lesser Malay chevrotain).		
OS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC		Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Tragulina;		
OC		Tragulidae; Tragulus.		
OX		NCBI_TaxID=9849;		
RN		[1]_TaxID=9849;		
RP		SEQUENCE FROM N.A.		
RP		MEDLINE=21347458; PubMed=11453981;		
RX		Breukelman H.J., Jekel P.A., Dubois J.Y., Mulder P.P.M.F.A.,		
RX		Warms H.W., Beintema J.J.;		
RT		"Secretory ribonucleases in the primitive ruminant chevrotain		
RT		(Tragulus javanicus)".		
RL		Bar. J. Biochem. 268:3890-3897(2001).		
CC		-!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.		
CC		EMBL; AJ271299; CAC24723.1; -.		
DR		HSP; P00656; 1LSQ.		
DR		GO; GO:0004519; F:endonuclease activity; IEA.		
DR		GO; GO:0016787; F:hydrolase activity; IEA.		
DR		GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.		
DR		InterPro; IPR001427; RNaseA.		
DR		Pfam; PF00074; rnaseA; 1.		
DR		PRINTS; PR00794; RIBONUCLEASE.		
DR		ProDom; PD000535; RNaseA; 1.		
DR		SMART; SM00092; RNase_Pc; 1.		
DR		PROSITE; PS00127; RNASE_PANCREATIC; 1.		
KW		Endonuclease; Hydrolase; Nuclease; Signal.		
FT	NON_TER	1		
FT	SIGNAL	<1	19	POTENTIAL.
FT	CHAIN	20	170	BRAIN-TYPE RIBONUCLEASE RIBONUCLEASE
SEQUENCE		170 AA:	18832 MW:	AB6CE7E1E5549AA0 CRC64.

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Query Match      21.6%; Score 131; DB 6; Length 170;  
Best Local Similarity 33.1%; Pred. No. 2.9e-07;  
Matches         41; Conservative    17; Mismatches   46; Indels     20; Gaps       7;
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QY    5   ATEQQKHI-----INTPIICNTMDNNIIVIGVCKRVNFTFISSATTVKAIT----- 53  
| | : : | |  
Db     25 AKPRRQLHDAGNSINS-YCNLMKKR-XMTHGRCKPVMTFIESLEDVKAI CSEKNIT 82  
| | : : | |

QY    54 ---GVINMMNVLSITRFOLNCTRTSITI PRP-CPIYSSTETNIYCVKEN---QYPVHFAGI 107  
| | : : | |

db    83 CKNGQPNCCHOSNET-MNII TCRGTGGSKYNCA YKTOKOYII I VACGEPTSPVPFHDSG 141  
| | : : | |

RESULT 15	
Q80285	PRELIMINARY; PRT; 144 AA.
ID	
AC	Q80285;
DT	01-JUN-2003 (TrEMBLrel. 24, Created)
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Angiogenin-4.
GN	ANG4.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=NMRI;
RX	MEDLINE=22493143; PubMed=12548285;

```

RA Hooper L.V., Stappenbeck T.S., Hong C.V., Gordon J.I.;
RT "Angiogenins: a new class of microbicidal proteins involved in innate
RI immunity.";
RL Nat. Immunol. 4:269-273(2003).
DR EMBL: AV219870; AAC62354.1; -.
DR GO: GO:0003676; F:nucleic acid binding; IEA.
DR GO: GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnaseA; 1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
SQ SEQUENCE 144 AA; 16554 MW; 09808807C00224C1 CRC64;

Query Match 21.2%; Score 128.5; DB 11; Length 144;
Best Local Similarity 38.2%; Pred.No.4.7e-07;
Matches 29; Conservative 13; Mismatches 29; Indels 5; Gaps 3;

QY 34 CKRVNTFIISATTVKAIC--TGVINMV-LSTTFQLNCTTSTTP-RPCPYSSRTE 88
Db 62 CKDVNTFIHGTKNIRALCKGKSGYNGENFRISNPFQITCTTSHRSGSPWPCGYRPFK 121
||| ||| : : ||| : : ||| : : ||| : : ||| : :
QY 89 TNYICVKCENQYVPHF 104
||| : ||| : |||
Db 122 FRVIVACEDGWPFVHF 137
||| : ||| : |||

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Search completed: May 7, 2004, 21:46:04  
Job time : 32.5659 secs

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RESULT 11
Q9DFY7 ID Q9DFY7 PRELIMINARY; PRT; 128 AA.
AC Q9DFY7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RC-Nase3 ribonuclease precursor.
OS Rana catesbeiana (bullfrog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1] SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104 (2000).
DR EMBL; AF242554; AAC31440.2; -.
DR HSSP; P22069; IONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SIGNAL.
FT CHAIN 1 23 POTENTIAL.
FT SIGNAL 24 128 RC-RNASE3 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14517 MM; 2B14986082E0587D CRC64;

Query Match 37.3%; Score 226.5; DB 13; Length 128;
Best Local Similarity 41.1%; Pred. No. 1.6e-18;
Matches 46; Conservative 18; Mismatches 39; Indels 9; Gaps 4;

QY 2 QNWATFQKHILNT-PIICNTIMNNIYVGGCKRVNTFISSATVKAICTGV-INNN 59
Db 24 QDMETFKKHLTDTKVKCDVEMKALF---DCKKNTFIYALPGRVKALCKNIRDNTD 79

QY 60 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 80 VLSDRAFLPQCDRIKL---PCHYKLSSNTITCIVNOLPHIFAGVGSCP 128

Query Match 37.3%; Score 226.5; DB 13; Length 128;
Best Local Similarity 41.1%; Pred. No. 1.6e-18;
Matches 46; Conservative 18; Mismatches 39; Indels 9; Gaps 4;

QY 2 QNWATFQKHILNT-PIICNTIMNNIYVGGCKRVNTFISSATVKAICTGV-INNN 59
Db 24 QDMETFKKHLTDTKVKCDVEMKALF---DCKKNTFIYALPGRVKALCKNIRDNTD 79

QY 60 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 80 VLSDRAFLPQCDRIKL---PCHYKLSSNTITCIVNOLPHIFAGVGSCP 128

RESULT 12
Q9DFY5 ID Q9DFY5 PRELIMINARY; PRT; 128 AA.
AC Q9DFY5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RC-Nase6 ribonuclease precursor.
OS Rana catesbeiana (bullfrog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1] SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104 (2000).
DR EMBL; AF242556; AAC31442.2; -.
DR HSSP; P22069; IONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SIGNAL.
FT CHAIN 1 23 POTENTIAL.
FT SIGNAL 24 128 RC-RNASE6 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14517 MM; 2B14986082E0587D CRC64;

Query Match 37.3%; Score 226.5; DB 13; Length 128;
Best Local Similarity 41.1%; Pred. No. 1.6e-18;
Matches 46; Conservative 18; Mismatches 39; Indels 9; Gaps 4;

QY 2 QNWATFQKHILNT-PIICNTIMNNIYVGGCKRVNTFISSATVKAICTGV-INNN 59
Db 24 QDMETFKKHLTDTKVKCDVEMKALF---DCKKNTFIYALPGRVKALCKNIRDNTD 79

QY 60 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 80 VLSDRAFLPQCDRIKL---PCHYKLSSNTITCIVNOLPHIFAGVGSCP 128

Query Match 37.3%; Score 226.5; DB 13; Length 128;
Best Local Similarity 41.1%; Pred. No. 1.6e-18;
Matches 46; Conservative 18; Mismatches 39; Indels 9; Gaps 4;

QY 2 QNWATFQKHILNT-PIICNTIMNNIYVGGCKRVNTFISSATVKAICTGV-INNN 59
Db 24 QDMETFKKHLTDTKVKCDVEMKALF---DCKKNTFIYALPGRVKALCKNIRDNTD 79

QY 60 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 80 VLSDRAFLPQCDRIKL---PCHYKLSSNTITCIVNOLPHIFAGVGSCP 128

RESULT 13
Q9W738 ID Q9W738 PRELIMINARY; PRT; 169 AA.
AC Q9W738;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PRL2 protein.
GN PRL2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1] SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RX MEDLINE=96069863; PubMed=7585965;
RA Kinoshita N., Minshull J., Kirschner M.W.;
RT "The identification of two novel ligands of the FGF receptor by a
yeast screening method and their activity in Xenopus development.";
RL Cell 83:621-630 (1995).
RN [2] SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RA Kinoshita N., Kirschner M.W.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF159166; AAD41901.1; -.
DR HSSP; P00656; ILSQ.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ SEQUENCE 169 AA; 18891 MM; D969F3E43BCE1B8 CRC64;

Query Match 26.9%; Score 163; DB 13; Length 169;
Best Local Similarity 39.3%; Pred. No. 5.3e-11;
Matches 44; Conservative 10; Mismatches 50; Indels 8; Gaps 6;

QY 2 QNWATFQKHIL--NTPICN-TIMNNIYVGGCKRVNTFI-SSATVKAICTGVIN 57
Db 28 QNINAFMEKHIVKEGAETNCNQIKDNRIF--KNCKFRNTFTDHTNGKKVEMCAGIVK 86

QY 58 MN-VLSTTRFQNLNCTRTSITPRP--CPYSSRTETNYICVKCENQYPVHFAG 106
Db 87 STFVSKELLPLTDCLLMGRTAPPCNAYNQITGTGTVINITCENNYVPVHFAG 138

RESULT 14

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RESULT 8
Q8UVX5
ID Q8UVX5 PRELIMINARY; PRT; 127 AA.
AC Q8UVX5;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Onconase precursor.
GN RPR.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Wang S.-C.;
RL "Rana pipiens onconase genomic DNA.";
RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332139; AAL54383.1; -.
DR FJ; A39035; A39035.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SIGNAL.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 127 AA; 14469 MW; 953F90D351CPEEF3 CRC64;

Query Match 45.7%; Score 277.5; DB 13; Length 127;
Best Local Similarity 49.5%; Pred. No. 1.7e-24;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 2 QNWATFOQKHINT-PIICNTIMDNNIYVGGCKRVNTFISSATTVAICTGVI-NMN 59
Db 24 QDWATFKKKHLTDWVDCDNLMTSLF---DCKQKNTFIYSLFPGPVKALCRGVIFSAD 79
QY 60 VLSTTRFQNLCTRTSITPR-PCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 80 VLTTSEFVLSDC---NVTSRCKYKLLKSTKFCVTCENQAPVHFVGVGSC 127

RESULT 9
Q9DFY6
ID Q9DFY6 PRELIMINARY; PRT; 129 AA.
AC Q9DFY6;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE RC-RNase4 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242553; AAG31441.2; -.
DR PDB; 1KVZ; 28-JUL-02.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.

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DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SIGNAL.
FT SIGNAL.
FT CHAIN 1 23 POTENTIAL.
SQ SEQUENCE 129 AA; 14724 MW; 826A62882B10ABDA CRC64;

Query Match 40.5%; Score 246; DB 13; Length 129;
Best Local Similarity 43.4%; Pred. No. 8.4e-21;
Matches 49; Conservative 24; Mismatches 30; Indels 10; Gaps 5;

QY 2 QNWATFOQKHINT-PIICNTIMDNNIYVGGCKRVNTFISSATTVAICTGVI-NMN 59
Db 24 QDWATFKKKHLTDWVDCDNLMTSLF---DCKQKNTFIYSLFPGPVKALCRGVIFSAD 79
QY 60 VLSTTRFQNLCTRTSITPR-PCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 80 VLSNSEFVLAEC---NVKPRKPKYKLLKSSNRICIRCEHLPVHFAGVIGICP 129

RESULT 10
Q9DFY8
ID Q9DFY8 PRELIMINARY; PRT; 128 AA.
AC Q9DFY8;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE RC-RNase2 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242553; AAG31439.1; -.
DR PDB; 1M58; 09-JAN-03.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SIGNAL.
FT SIGNAL.
FT CHAIN 1 23 POTENTIAL.
SQ SEQUENCE 128 AA; 14839 MW; 989719CF52053ECC CRC64;

Query Match 37.8%; Score 229.5; DB 13; Length 128;
Best Local Similarity 40.2%; Pred. No. 7e-19;
Matches 45; Conservative 20; Mismatches 38; Indels 9; Gaps 4;

QY 2 QNWATFOQKHINT-PIICNTIMDNNIYVGGCKRVNTFISSATTVAICTGVI-NMN 59
Db 24 QNWATFKKKHLTDWVDCDNLMTSLF---DCKQKNTFIYSLFPGPVKALCRGVIFSAD 79
QY 60 VLSTTRFQNLCTRTSITPR-PCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 80 VLSTDEFYLSDCNRKIL---PCHYKLLKSSNTTICENKLPVHFVAVEECP 128

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[illegible]

[illegible]

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:10 ; Search time 31.566 Seconds

(without alignments)  
1109.503 Million cell updates/sec

Title: US-09-961-400-17

Perfect score: 607

Sequence: 1 MNWATFOQRHINTPIICN.....ICVKCENQYVHPFAGIGRCP 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_25:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_rvirus:\*

16: sp\_bacteriap:\*

17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	560.5	92.3	133	13	Q98SM0 rana catesb
2	487.5	80.3	132	13	Q98SM2 rana catesb
3	478.5	78.8	133	13	Q98SL9 rana catesb
4	471.5	77.7	133	13	Q98SL8 rana catesb
5	448.5	73.9	132	13	Q98SM1 rana catesb
6	376	61.9	132	13	Q9DF78 rana catesb
7	281.5	46.4	127	13	Q918V8 rana pipien
8	277.5	45.7	127	13	Q8UUX5 rana pipien
9	246	40.5	129	13	Q9DFY6 rana pipien
10	229.5	37.8	128	13	Q9DFY8 rana catesb
11	226.5	37.3	128	13	Q9DFY7 rana catesb
12	217.5	35.8	128	13	Q9DFY5 rana catesb
13	163	26.9	169	13	Q9W738 xenopus lae
14	131	21.6	170	6	Q9BEC1 tragulus ja
15	128.5	21.2	144	11	Q80Z85 mus musculus
16	128.5	21.2	153	11	Q80XS4 mus musculus

17	127.5	21.0	147	6	Q7VRJ6	Q7vrj6 balaena mys
18	126	20.8	150	11	Q8VD94	Q8vd94 berylmys bo
19	125.5	20.7	163	6	Q9BDC2	Q9bdc2 antilocapra
20	124.5	20.5	116	6	Q9TVCO	Q9tvco sus scrofa
21	124	20.4	150	11	Q8VD88	Q8vd88 rattus norv
22	122.5	20.2	144	6	Q9BH14	Q9bh14 antilocapra
23	121.5	20.0	147	6	Q7VRJ5	Q7vrj5 tursiops tr
24	121	19.9	146	6	Q861Y5	Q861y5 colobus gue
25	120.5	19.9	149	11	Q8K2T2	Q8k2t2 mus musculu
26	120.5	19.9	149	11	Q8CG63	Q8c6g3 mus musculu
27	120	19.8	150	11	Q8VD92	Q8vd92 rattus exul
28	119.5	19.7	146	6	Q861Y4	Q861y4 trachypithe
29	118.5	19.5	146	6	Q861Y3	Q861y3 pygathrix r
30	118.5	19.5	146	6	Q861Y2	Q861y2 pygathrix b
31	118.5	19.5	146	6	Q861Y1	Q861y1 pygathrix a
32	116.5	19.2	152	11	Q8VD89	Q8vd89 rattus norv
33	114.5	18.9	124	6	Q9SNE6	Q9sne6 bubalus bub
34	112.5	18.5	148	11	Q8C7E4	Q8c7e4 mus musculu
35	112.5	18.5	149	11	Q8VD95	Q8vd95 berylmys bo
36	112	18.5	134	6	Q9BDB9	Q9bdb9 tragulus ja
37	111.5	18.4	152	11	Q8VD84	Q8vd84 rattus tiom
38	111.5	18.4	156	6	Q8SQ05	Q8sq05 lagothrix l
39	111	18.3	148	11	Q8C663	Q8c663 mus musculu
40	110.5	18.2	119	6	Q9TV28	Q9tv28 eulemur ful
41	110.5	18.2	119	6	Q9TV30	Q9tv30 saguinus oe
42	109.5	18.0	142	6	Q9BEC3	Q9bec3 tragulus ja
43	109.5	18.0	156	6	Q8SQ06	Q8sq06 ateles geof
44	109	18.0	124	6	Q9BEC2	Q9bec2 tragulus ja
45	108.5	17.9	156	6	Q8SQ08	Q8sq08 salmirel sci

## ALIGNMENTS

### RESULT 1

Q98SM0 PRELIMINARY; PRT; 133 AA.  
AC Q98SM0;  
DT 01-JUN-2001 (TREMREL. 17, Created)  
DT 01-JUN-2001 (TREMREL. 17, Last sequence update)  
DE RNase A-type ribonuclease rc208 precursor.  
OS Rana catesbeiana (Bull frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
OX NCBI\_TaxID=8400;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21539506; PubMed=11683320;  
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;  
RT "Rapid diversification of RNase A superfamily ribonuclease from the  
bullfrog, Rana catesbeiana.";  
RL J. Mol. Evol. 53:31-38(2001).  
DR HSSP; P11916; 18C4.  
DR GO; GO:0003676; F:nucleic acid binding; IEA.  
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.  
DR InterPro; IPR001427; RNaseA.  
DR Pfam; PF00074; rnasea; 1.  
DR ProDom; PD000535; RNaseA; 1.  
DR SMART; SM00092; RNase Pc; 1.  
DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
KW Signal.  
FT SIGNAL.  
SQ SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;

Query Match 92.3%; Score 560.5; DB 13; Length 133;  
Best Local Similarity 94.6%; Pred. No. 1.8e-57;  
Matches 105; Conservative 0; Mismatches 5; Indels 1; Gaps 1;  
Qy 2 QNWATFOQRHINTPII-CNTIMDNNTIYVGQCKRVNTFISSATTVKALCTGVINNV 60  
Db 23 QNWATFOQRHINTPII-CNTIMDNNTIYVGQCKRVNTFISSATTVKALCTGVINNV 82

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Q9JKI5
ID Q9JKI5 PRELIMINARY; PRT; 152 AA.
AC Q9JKI5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Eosinophil-associated ribonuclease 10.
GN EAR10.
OS Mus saxicola (Spiny mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10094;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20243759; PubMed=10758160;
RA Zhang J., Dyer K.D., Rosenberg H.F.;
RT "Evolution of the rodent eosinophil-associated ribonuclease gene
RT family by rapid gene sorting and positive selection.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).
DR EMBL; AF238398; AAF67698.1; -.
DR HSSP; P10153; IH12.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Fc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ SEQUENCE 152 AA; 16830 MW; 780421C3661732C8 CRC64;

Query Match 22.9%; Score 133; DB 11; Length 152;
Best Local Similarity 30.3%; Pred. No. 2e-07;
Matches 37; Conservative 19; Mismatches 42; Indels 24; Gaps 6;

Qy 2 SDWLTFOKKHLTNTRDVCNNIM---STNLFPHCKDKNTFIYSRPEPVKAIC---KGIIA- 54
Db 31 SQW--FATQHTNTANPCQVEMLPINRNRRCNINFTLHFPANVVGCGNPSGLCSN 88

Qy 55 --SKNVLTTSEFYLSDCNVTSR-----PCKYKLKSTNTFCVTCENQAP-----VHF 99
Db 89 NISTNCHNSSRPVITVCNITTSREKSTQCRVYQKGSVEYTVACNPRTPQDSRPYPVHL 148

Qy 100 VG 101
Db 149 DG 150

RESULT 15
Q9JKI9
ID Q9JKI9 PRELIMINARY; PRT; 157 AA.
AC Q9JKI9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Eosinophil-associated ribonuclease 44.
GN EAR44.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20243759; PubMed=10758160;
RA Zhang J., Dyer K.D., Rosenberg H.F.;
RT "Evolution of the rodent eosinophil-associated ribonuclease gene
RT family by rapid gene sorting and positive selection.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).
DR EMBL; AF238394; AAF67694.1; -.
DR HSSP; P10153; IH12.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
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DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Fc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ SEQUENCE 157 AA; 17887 MW; 34FE2AE777EF3709 CRC64;

Query Match 22.5%; Score 131; DB 11; Length 157;
Best Local Similarity 30.6%; Pred. No. 3.5e-07;
Matches 34; Conservative 20; Mismatches 37; Indels 20; Gaps 7;

Qy 2 SDWLTFOKKHLTNTRDVCNNIM---STNLF--HCKDKNTFIYSRPEPV-----KAICKG 51
Db 34 SQWFTIQ--HISNTTTIQCNAALGVNNYTGRCCKDLNFTLHTRFANVVNVCYNNTTCKN 91

Qy 52 IIAASKNVL--TTSEFYLSDCNVTS-----RPCKYKLKSTNTFCVTCENQAP 96
Db 92 --GRRNCHDSRSKVSITDCLNLTSPSANYRQCRVYQTRARFYRIACNNKTP 140

Search completed: May 7, 2004, 21:46:03
Job time : 30.8597 secs
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## RESULT 14





```
Db 25 NWETFQKKHLTDTRVDCKDAEMKALFDCKQKNTFIYARPRVQALCKNIIVSKNVLSTD 84
QY 63 EFYLSDCNVTSPCKYKLLKSTNTFCVTENQAPVHFVGVC 105
Db 85 EFYLSDCNRIKLPCHYKLLKSSNTICITCENKLPVHFVAVEEC 127

RESULT 5
Q9DFY7 PRELIMINARY; PRT; 128 AA.
AC Q9DFY7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RC-RNase3 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104 (2000).
DR EMBL; AF242554; AAG31440.2; -.
DR HSSP; P22069; IONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SIGNAL.
KW SIGNAL.
FT CHAIN 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNASE6 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14517 MW; 2B14986082E50587D CRC64;

Query Match 52.6%; Score 306; DB 13; Length 128;
Best Local Similarity 54.4%; Pred. No. 1.9e-27;
Matches 56; Conservative 12; Mismatches 35; Indels 0; Gaps 0;

QY 3 DWLTFQKKHLTDTRVDCKNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 62
Db 25 DWLTFQKKHLTDTRVKKCDVEMKALFDCKKNTFIYALFGRVKALCKNIRDNTDVLSD 84
QY 63 EFYLSDCNVTSPCKYKLLKSTNTFCVTENQAPVHFVGVC 105
Db 85 AFLPQCDRIKLPCHYKLLKSSNTICITCENQLPVHFVAGVGC 127

RESULT 6
Q9DFY5 PRELIMINARY; PRT; 128 AA.
AC Q9DFY5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RC-RNase6 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104 (2000).
DR EMBL; AF242554; AAG31440.2; -.
DR HSSP; P22069; IONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SIGNAL.
KW SIGNAL.
FT CHAIN 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNASE3 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14517 MW; 2B14986082E50587D CRC64;

Query Match 52.6%; Score 306; DB 13; Length 128;
Best Local Similarity 54.4%; Pred. No. 1.9e-27;
Matches 56; Conservative 12; Mismatches 35; Indels 0; Gaps 0;

QY 3 DWLTFQKKHLTDTRVDCKNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 62
Db 25 DWLTFQKKHLTDTRVKKCDVEMKALFDCKKNTFIYALFGRVKALCKNIRDNTDVLSD 84
QY 63 EFYLSDCNVTSPCKYKLLKSTNTFCVTENQAPVHFVGVC 105
Db 85 AFLPQCDRIKLPCHYKLLKSSNTICITCENQLPVHFVAGVGC 127

RESULT 7
Q98SM0 PRELIMINARY; PRT; 133 AA.
AC Q98SM0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=21539506; PubMed=11683320;
RX Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38 (2001).
DR EMBL; AF351209; AAK30255.1; -.
DR HSSP; P11916; IBC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT SIGNAL.
SQ SEQUENCE 133 AA; 14628 MW; 87FCF12C3499E02 CRC64;

Query Match 50.3%; Score 293; DB 13; Length 133;
Best Local Similarity 49.1%; Pred. No. 6.1e-26;
Matches 54; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

QY 3 DWLTFQKKHLTDTRVDCKNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNV 58
Db 24 NWATFQKKHLTDTRSSINCNTIMDNNTIYGVGGQCKGNTFISSATVKAICTGVI-NNNV 82
QY 59 LTTSEFYLSDC---NVTSPCKYKLLKSTNTFCVTENQAPVHFVGVC 105
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```
RL Nucleic Acids Res. 28:4097-4104 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242556; AAG31442.2; -.
DR HSSP; P22069; IONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT SIGNAL.
SQ SEQUENCE 128 AA; 14804 MW; AFE9FD67D266C7C2 CRC64;

Query Match 52.2%; Score 304; DB 13; Length 128;
Best Local Similarity 53.4%; Pred. No. 3.2e-27;
Matches 55; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

QY 3 DWLTFQKKHLTDTRVDCKNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 62
Db 25 DWLTFQKKHLTDTRVKKCDVEMKALFDCKKNTFIYALFGRVKALCKNIRDNTDVLSD 84
QY 63 EFYLSDCNVTSPCKYKLLKSTNTFCVTENQAPVHFVGVC 105
Db 85 VFYLPQCNRRKLPCHYRLDGSNTICITCMKELPIHFAGVGKC 127

RESULT 7
Q98SM0 PRELIMINARY; PRT; 133 AA.
AC Q98SM0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=21539506; PubMed=11683320;
RX Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38 (2001).
DR EMBL; AF351209; AAK30255.1; -.
DR HSSP; P11916; IBC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT SIGNAL.
SQ SEQUENCE 133 AA; 14628 MW; 87FCF12C3499E02 CRC64;

Query Match 50.3%; Score 293; DB 13; Length 133;
Best Local Similarity 49.1%; Pred. No. 6.1e-26;
Matches 54; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

QY 3 DWLTFQKKHLTDTRVDCKNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNV 58
Db 24 NWATFQKKHLTDTRSSINCNTIMDNNTIYGVGGQCKGNTFISSATVKAICTGVI-NNNV 82
QY 59 LTTSEFYLSDC---NVTSPCKYKLLKSTNTFCVTENQAPVHFVGVC 105
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Db 25 DMLTFQKKHLINTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 84

QY 63 EFYLSDCNVTSRPCKYKLLKXSTNTFCVTCENQAPVHFVGSHC 105

Db 85 EFYLSDCNVTSRPCKYKLLKXSTNTFCVTCENQAPVHFVGSHC 127

RESULT 2  
Q8UX5 PRELIMINARY; PRT; 127 AA.

ID Q8UX5 AC Q8UX5;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
TT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Onconase precursor.  
GN RPR.

OS Rana pipiens (Northern leopard frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OX Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
NCBI\_TaxID=8404;  
[1] RN SEQUENCE FROM N.A.  
RP Liao Y.-D., Wang S.-C.;  
RA "Rana pipiens onconase genomic DNA.";  
RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF332139; AAL54383.1; -;  
DR PIR; A39035; A39035.  
DR GO; GO:0003676; F:nucleic acid binding; IEA.  
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.  
DR InterPro; IPR001427; RNASEA.  
DR Pfam; PF00074; rnaseA; 1.  
DR ProDom; PD000535; RNaseA; 1.  
DR SMART; SM00092; RNase PG; 1.  
DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
KW Signal.  
FT SIGNAL.  
SQ SEQUENCE 1 23 POTENTIAL.  
SEQUENCE 127 AA; 14469 MW; 953F90D351CFEEF3 CRC64;

Query Match 94.7%; Score 551; DB 13; Length 127;  
Best Local Similarity 96.1%; Pred. No. 1e-55; Gaps 0;  
Matches 99; Conservative 2; Mismatches 2; Indels 0; Gaps 0

QY 3 DMLTFQKKHLINTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 62

Db 25 DMLTFQKKHLINTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 84

QY 63 EFYLSDCNVTSRPCKYKLLKXSTNTFCVTCENQAPVHFVGSHC 105

Db 85 EFYLSDCNVTSRPCKYKLLKXSTNTFCVTCENQAPVHFVGSHC 127

RESULT 3  
Q9DFY6 PRELIMINARY; PRT; 129 AA.

ID Q9DFY6 AC Q9DFY6;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
TT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE RC-Rnase4 ribonuclease precursor.  
OS Rana catesbeiana (Bull frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OX Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
NCBI\_TaxID=8400;  
[1] RN SEQUENCE FROM N.A.  
RP TISSUE=Liver;  
RA MEDLINE=20512555; PubMed=11059105;  
QY Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;  
RT "Purification and cloning of cytotoxic ribonucleases from Rana  
catesbeiana (bullfrog).";  
RL Nucleic Acids Res. 28:4097-4104(2000).  
RN [2]

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:10 ; Search time 29.8597 Seconds  
(without alignments)  
1109.503 Million cell updates/sec

Title: US-09-961-400-13  
Perfect score: 582  
Sequence: 1 MSDWLTFOKKHLNTRDVC.....TFCVTCENQAPVHFVGVGHC 105

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25: \*  
1: sp\_archaea: \*  
2: sp\_bacteria: \*  
3: sp\_fungi: \*  
4: sp\_human: \*  
5: sp\_invertebrate: \*  
6: sp\_mammal: \*  
7: sp\_mhc: \*  
8: sp\_organelle: \*  
9: sp\_phase: \*  
10: sp\_plant: \*  
11: sp\_rodent: \*  
12: sp\_virus: \*  
13: sp\_vertebrate: \*  
14: sp\_unclassified: \*  
15: sp\_rvirus: \*  
16: sp\_bacteriap: \*  
17: sp\_archaeap: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	573	98.5	127	13	Q918V8
2	551	94.7	127	13	Q8UVX5
3	399.5	68.6	128	13	Q9DFV6
4	381	65.5	129	13	Q9DFV8
5	306	52.6	128	13	Q9DFV7
6	304	52.2	128	13	Q9DFV5
7	293	50.3	133	13	Q98SM0
8	281	48.3	132	13	Q98SM2
9	281	48.3	133	13	Q98SL9
10	277	47.6	133	13	Q98SL8
11	275	47.3	132	13	Q98SM1
12	270.5	46.5	132	13	Q9DFV8
13	157.5	27.1	169	13	Q9W738
14	133	22.9	152	11	Q9JKI5
15	131	22.5	157	11	Q9JKI9
16	130.5	22.4	153	11	Q9JKI7

17	130	22.3	157	11	Q9UKJ3
18	128.5	22.1	146	6	Q861Y3
19	128.5	22.1	146	6	Q861Y2
20	128.5	22.1	146	6	Q861Y1
21	127	21.8	154	11	Q9UKI8
22	127	21.8	157	11	Q9UKJ4
23	126	21.6	157	11	Q9UKJ1
24	125	21.5	157	11	Q9UKJ2
25	124.5	21.4	146	6	Q861Y4
26	124.5	21.4	155	11	Q9UKH9
27	123.5	21.2	155	11	Q9UKI3
28	121	20.8	147	6	Q7YRJ6
29	120.5	20.7	155	11	Q9UKI6
30	119.5	20.5	155	11	Q9UKI2
31	119.5	20.5	155	11	Q9UKI4
32	118	20.3	147	6	Q7YRJ5
33	117.5	20.2	155	11	Q9UKI34
34	117	20.1	156	11	Q9UKG6
35	117	20.1	156	11	Q9UKH7
36	116.5	20.0	132	6	Q9TV25
37	116.5	20.0	132	6	Q9TV24
38	116.5	20.0	155	11	Q9RI25
39	116.5	20.0	155	11	Q9UKH8
40	116	19.9	156	11	Q9UKG7
41	115	19.8	146	6	Q861Y5
42	115	19.8	156	11	Q9UKH4
43	115	19.8	156	11	Q9UKG9
44	115	19.8	156	11	Q9UKH5
45	114.5	19.7	170	6	Q9BEC1

## ALIGNMENTS

## RESULT 1

Q918V8 PRELIMINARY; PRT; 127 AA.  
ID Q918V8  
AC Q918V8;  
DT 01-OCT-2000 (TREMUREL. 15, Created)  
DT 01-OCT-2000 (TREMUREL. 15, Last sequence update)  
DT 01-OCT-2003 (TREMUREL. 25, Last annotation update)  
DE Onconase variant rapR1 precursor.  
OS Rana pipiens (Northern leopard frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
RX NCBI\_taxID=8404;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
EX MEDLINE=20330357; PubMed=10871370;  
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;  
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a 3' UTR of unusual length and structure."  
RL Nucleic Acids Res. 28:2375-2382(2000).  
DR EMBL; AF165133; AAF76935.1; -  
DR PIR; A39035; A39035.  
DR HSP; P22069; 10NC.  
DR GO; GO:0003676; F:nucleic acid binding; IEA.  
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.  
DR InterPro; IPR001427; RNaseA.  
DR Pfam; PF00074; rnaseA; 1.  
DR ProDom; PD000535; RNaseA; 1.  
DR SMART; SM00092; RNase\_P; 1.  
DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
KW Signal.  
FT SIGNAL.  
SQ SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;

Query Match 98.5%; Score 573; DB 13; Length 127;

Best Local Similarity 100.0%; Pred. No. 3e-58; Indels 0; Gaps 0;  
Matches 103; Conservative 0; Mismatches 0;

QY 3 DWLTFQKKHLNTRDVCNINMSTNLFHCKDKNTFYGRPEPVKAICKGIASKNVLTTTS 62

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Q9JKI5
ID Q9JKI5 PRELIMINARY; PRT; 152 AA.
AC Q9JKI5;
DC 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Eosinophil-associated ribonuclease 10.
GN EAR10.
OS Mus saxicola (Spiny mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10094;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20243759; PubMed=10758160;
RA Zhang J., Dyer K.D., Rosenberg H.F.;
RT "Evolution of the rodent eosinophil-associated ribonuclease gene
RT family by rapid gene sorting and positive selection.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).
DR EMBL; AF238398; AAF67698.1; -.
DR HSSP; P10153; IHI2.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA.
DR PRINTS; PR00794; RIBONUCLEASE.
DR PRODOM; PR000535; RNaseA; 1.
DR SMART; SM00092; RNasePc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ SEQUENCE 152 AA; 16830 MW; 780421C3661732C8 CRC64;

Query Match 23.1%; Score 133; DB 11; Length 152;
Best Local Similarity 30.3%; Pred. No. 1.8e-07;
Matches 37; Conservative 19; Mismatches 42; Indels 24; Gaps 6;

Qy 1 SDWLTFFQKKHLNTRDVCNNIM---STNLFCKDKNTFIYSRPEPVKAIC---KGIIA- 53
Db 31 SQW--FATQHTNTANPCNVEMLPINENRTCKNINFLHTFANVVGVCGNPSGLCSN 88

Qy 54 --SKVLTTSEFYLSDCNVTSR----PCKYKLLKSTNFCVTCENQAP-----VHF 98
Db 89 NISTCHNSRRVPTVCNITREKSKTQCRVQTKGSVEYTVACNPRTPQDSPPYVHL 148

Qy 99 VG 100
Db 149 DG 150

RESULT 15
Q9JKI9
ID Q9JKI9 PRELIMINARY; PRT; 157 AA.
AC Q9JKI9;
DC 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Eosinophil-associated ribonuclease 44.
GN EAR44.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20243759; PubMed=10758160;
RA Zhang J., Dyer K.D., Rosenberg H.F.;
RT "Evolution of the rodent eosinophil-associated ribonuclease gene
RT family by rapid gene sorting and positive selection.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).
DR EMBL; AF238394; AAF67694.1; -.
DR HSSP; P10153; IHI2.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.

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DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR PRODOM; PR000535; RNaseA; 1.
DR SMART; SM00092; RNasePc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ SEQUENCE 157 AA; 17887 MW; 34FE2AE777EEF3709 CRC64;

Query Match 22.7%; Score 131; DB 11; Length 157;
Best Local Similarity 30.6%; Pred. No. 3.2e-07;
Matches 34; Conservative 20; Mismatches 37; Indels 20; Gaps 7;

Qy 1 SDWLTFFQKKHLNTRDVCNNIM---STNLF--HCKDKNTFIYSRPEPV-----KAICKG 50
Db 34 SQWFTIQ--HISNTTTICNAAMLGVNNYTGCKDLNLTFLHTFANVVVNECYNRTTCKN 91

Qy 51 IIAKKNVL--TTSEFYLSDCNVTS-----RCKYKLLKSTNFCVTCENQAP 95
Db 92 --GRNCHDSRSKVSITDCNLTSPSANYRQCRVQTRARFYRIACNNKTP 140

Search completed: May 7, 2004, 21:46:02
Job time : 29.5753 secs

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DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaase; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 132 RC-RNASEI1 RIBONUCLEASE.
SQ SEQUENCE 132 AA; 14625 MW; D8D9A517452FBE53 CRC64;

Query Match 46.9%; Score 270.5; DB 13; Length 132;
Best Local Similarity 43.6%; Pred. No. 2e-23;
Matches 48; Conservative 19; Mismatches 36; Indels 7; Gaps 3

QY 2 DWLTFQKKHLTNTRVDCCNNIMSTWLF----HCKDKNTFIYSRPPVKAICKGIISKNV 57
   :|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::
Db 23 NNAKFKKHITSSIDCNCNTMDKAIYIVGGKCKERNFTFIISSEDNVAICSGVSPDRKE 82

QY 58 LTTSEFLSDC---NVTSRPCKYLKKSNTFCVTCENQAPVHFVGVGHC 104
   ::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||
Db 83 LSTTSFKLNTCTRDSITPRPCBHPSPDNPKVCACEKQLPVHFGVGKC 132


RESULT 13
Q9W738 PRELIMINARY; PRT; 169 AA.
AC Q9W738;
DC Q9W738;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FRL2 protein.
GN FRL2
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxId=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96069863; PubMed=7585965;
RA Kinoshita N., Minshull J., Kirschner M.W.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
RE ENBL; AF159166; AAD41901.1; -.
DR HSSP; P00656; ILSQ.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaase; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ SEQUENCE 169 AA; 18891 MW; D969F3E43B3CE1B8 CRC64;

Query Match 27.3%; Score 157.5; DB 13; Length 169;
Best Local Similarity 36.1%; Pred. No. 3e-10;
Matches 39; Conservative 19; Mismatches 35; Indels 15; Gaps 3

QY 6 FQKKHLTNT-RDVDCN-----NIMSTNLFHCKDKNTFIY-SRPPVKAICKGIISKNV 57
   :|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||
Db 33 FMEXHIVKGEAGTENCQTIKDRNIIRPKN--NCKFRNTFIHDNTGKKVKEMCAGIVKSTFV 90

QY 58 LTTSEFLSDCNV---TSRP--CKYKLKKSNTFCVTCENQAPVHFVG 100
   ::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||
Db 91 ISKELPLTDCLMGHTAPPNCAYNQIFTTGVINICTENYTVHFAG 138


RESULT 14

```

Db 83 LSTRFQNTCTRTSITPRPCPYSSRTNNYICVKCNQYVPHFAGIGRC 132

RESULT 8

Q98SM2 PRELIMINARY; PRT; 132 AA.

AC Q98SM2; ID Q98SM2; DT 01-JUN-2001 (TReMBLrel. 17, Created)

DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)

DE RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).

OS Rana catesbeiana (Bull frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.

OC NCBI\_TaxID=8400;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21539506; PubMed=11683320;

RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;

RT "Rapid diversification of RNase A superfamily ribonuclease from the

RT bullfrog, *Rana catesbeiana*."

RL J. Mol. Evol. 53:31-38(2001).

RN [2]

RP SEQUENCE FROM N.A.

RQ TISSUE=Liver;

RC Liao Y.-D., Tang P.-C., Jeng J.-T.;

RA Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF351207; AAK30253.1; -

DR EMBL; AF359578; AAL67036.1; -

DR HSSP; P11916; IBC4.

DR GO; GO:0003676; F:nucleic acid binding; IEA.

DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.

DR InterPro; IPR001427; RNaseA.

DR Pfam; PF00074; rnaseA; 1.

DR ProDom; PD000535; RNaseA; 1.

DR SMART; SM00092; RNase\_PC; 1.

DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.

DR Signal.

KW SIGNAL.

FT CHAIN 1 22 POTENTIAL.

FT SIGNAL 23 132 RC-RNASE7.

SQ SEQUENCE 132 AA; 14412 MW; 131A745187978687 CRC64;

Query Match 48.7%; Score 281; DB 13; Length 132;

Best Local Similarity 47.7%; Pred. No. 1.2e-24;

Matches 52; Conservative 14; Mismatches 35; Indels 8; Gaps 3;

QY 3 WLFQKHLTNTRDVDCNNIMSTNLF---HCKDKNTFYSRPEPVKAICKGIASKNV 58

Db 25 WAKFQKHPTSSINCNTIMDNIIYVGGCKKNTFISSATTVAICNG-VTNSNV 83

QY 59 TTFSEFVLSDC---NVTSPCKYKLKSTNTFCVTNCNQAPVHFVGVC 104

Db 84 SPTRFQDLCTRTSITPRPCPYSSKKTNKICVKCNQLPVHFGIGRC 132

RESULT 9

Q98SL9 PRELIMINARY; PRT; 133 AA.

AC Q98SL9; ID Q98SL9; DT 01-JUN-2001 (TReMBLrel. 17, Created)

DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)

DE RNase A-type ribonuclease rc212 precursor.

OS Rana catesbeiana (Bull frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.

OC NCBI\_TaxID=8400;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21539506; PubMed=11683320;

RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;

RT "Rapid diversification of RNase A superfamily ribonuclease from the

RT bullfrog, *Rana catesbeiana*."

RL J. Mol. Evol. 53:31-38(2001).

RN [1]

RP SEQUENCE FROM N.A.

RQ TISSUE=Liver;

RC Liao Y.-D., Tang P.-C., Jeng J.-T.;

RA Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF351207; AAK30253.1; -

DR EMBL; AF359578; AAL67036.1; -

DR HSSP; P11916; IBC4.

DR GO; GO:0003676; F:nucleic acid binding; IEA.

DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.

DR InterPro; IPR001427; RNaseA.

DR Pfam; PF00074; rnaseA; 1.

DR ProDom; PD000535; RNaseA; 1.

DR SMART; SM00092; RNase\_PC; 1.

DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.

DR Signal.

KW SIGNAL.

FT CHAIN 1 22 POTENTIAL.

FT SIGNAL 23 132 RC-RNASE7.

SQ SEQUENCE 132 AA; 14412 MW; 131A745187978687 CRC64;

Query Match 48.7%; Score 281; DB 13; Length 132;

Best Local Similarity 47.7%; Pred. No. 1.2e-24;

Matches 52; Conservative 14; Mismatches 35; Indels 8; Gaps 3;

QY 3 WLFQKHLTNTRDVDCNNIMSTNLF---HCKDKNTFYSRPEPVKAICKGIASKNV 58

Db 25 WAKFQKHPTSSINCNTIMDNIIYVGGCKKNTFISSATTVAICNG-VTNSNV 83

QY 59 TTFSEFVLSDC---NVTSPCKYKLKSTNTFCVTNCNQAPVHFVGVC 104

Db 84 SPTRFQDLCTRTSITPRPCPYSSKKTNKICVKCNQLPVHFGIGRC 132

RESULT 9

Q98SL9 PRELIMINARY; PRT; 133 AA.

AC Q98SL9; ID Q98SL9; DT 01-JUN-2001 (TReMBLrel. 17, Created)

DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)

DE RNase A-type ribonuclease rc212 precursor.

OS Rana catesbeiana (Bull frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.

OC NCBI\_TaxID=8400;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21539506; PubMed=11683320;

RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;

RT "Rapid diversification of RNase A superfamily ribonuclease from the

RT bullfrog, *Rana catesbeiana*."

RL J. Mol. Evol. 53:31-38(2001).

RN [1]

RP SEQUENCE FROM N.A.

RQ TISSUE=Liver;

RC Liao Y.-D., Tang P.-C., Jeng J.-T.;

RA Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF351207; AAK30253.1; -

DR EMBL; AF359578; AAL67036.1; -

DR HSSP; P11916; IBC4.

DR GO; GO:0003676; F:nucleic acid binding; IEA.

DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.

DR InterPro; IPR001427; RNaseA.

DR Pfam; PF00074; rnaseA; 1.

DR ProDom; PD000535; RNaseA; 1.

DR SMART; SM00092; RNase\_PC; 1.

DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.

DR Signal.

KW SIGNAL.

FT CHAIN 1 22 POTENTIAL.

FT SIGNAL 23 132 RC-RNASE7.

SQ SEQUENCE 132 AA; 14412 MW; 131A745187978687 CRC64;

Query Match 48.7%; Score 281; DB 13; Length 133;

Best Local Similarity 46.4%; Pred. No. 3.6e-24;

Matches 51; Conservative 18; Mismatches 33; Indels 8; Gaps 3;

QY 2 DNLTFQKHLTNTRDVDCNNIMSTNLF---HCKDKNTFYSRPEPVKAICKGIASKNV 57

Db 24 NWATFQEGHITNTSSINCNNIMNSLYVGGCKKNTFIASSATTVKIGCSG-VTDKKV 82

QY 58 LTTSEFVLSDCN---VTSRCPCKYKLKSTNTFCVTNCNQAPVHFVGVC 104

Db 83 LSSTKFOLDICTRIFITPRPCPYSSRTETNYICVKCNQYVPHFAGIGQC 132

RESULT 10

Q98SL8 PRELIMINARY; PRT; 133 AA.

AC Q98SL8; ID Q98SL8; DT 01-JUN-2001 (TReMBLrel. 17, Created)

DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)

DE RNase A-type ribonuclease rc218 precursor.

OS Rana catesbeiana (Bull frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.

OC NCBI\_TaxID=8400;

RN [1]

RP SEQUENCE FROM N.A.

RQ TISSUE=Liver;

RC Liao Y.-D., Tang P.-C., Jeng J.-T.;

RA Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF351207; AAK30253.1; -

DR EMBL; AF359578; AAL67036.1; -

DR HSSP; P11916; IBC4.

DR GO; GO:0003676; F:nucleic acid binding; IEA.

DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.

DR InterPro; IPR001427; RNaseA.

DR Pfam; PF00074; rnaseA; 1.

DR ProDom; PD000535; RNaseA; 1.

DR SMART; SM00092; RNase\_PC; 1.

DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.

DR Signal.

KW SIGNAL.

FT CHAIN 1 22 POTENTIAL.

FT SIGNAL 23 132 RC-RNASE7.

SQ SEQUENCE 133 AA; 14615 MW; C8785B236B26E54E CRC64;

Query Match 48.7%; Score 281; DB 13; Length 133;

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Db 25 NMEFTQKKHLTDTRDKVCKDAEMKALFDCKQKNTFIYARPRVOALCKNIIVSKNVLSTD 84
Qy 62 EFLVSDCNVTSRCKYKLKSTNTFCVTCENQAPVHFVGVGHC 104
Db 85 EFLVSDCNRIKLPCHYKLLKSSNTICITCENKLPVHFVAVEEC 127

RESULT 5
Q9DFY7 PRELIMINARY; PRT; 128 AA.
ID Q9DFY7
AC Q9DFY7;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE RC-RNase3 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
DR EMBL; AF242554; AAG31440.2; -.
DR HSSP; P22069; 10NC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;

Query Match 53.0%; Score 306; DB 13; Length 128;
Best Local Similarity 54.4%; Pred. No. 1.5e-27;
Matches 56; Conservative 12; Mismatches 35; Indels 0; Gaps 0;

Qy 2 DMLTFQKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLTS 61
Db 25 DWETFQKKHLTDTRDKVCKDAEMKALFDCKKNTFIYALPGRVKALCKNIRDNTDVLSD 84

Qy 62 EFLVSDCNVTSRCKYKLKSTNTFCVTCENQAPVHFVGVGHC 104
Db 85 AFLPQCDRIKLPCHYKLLKSSNTICITCVNQLPIHFAGVGC 127

RESULT 6
Q9DFY5 PRELIMINARY; PRT; 128 AA.
ID Q9DFY5
AC Q9DFY5;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE RC-RNase6 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
DR EMBL; AF242554; AAG31440.2; -.
DR HSSP; P22069; 10NC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;

Query Match 53.0%; Score 306; DB 13; Length 128;
Best Local Similarity 54.4%; Pred. No. 1.5e-27;
Matches 56; Conservative 12; Mismatches 35; Indels 0; Gaps 0;

Qy 2 DMLTFQKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLTS 61
Db 25 DWETFQKKHLTDTRDKVCKDAEMKALFDCKKNTFIYALPGRVKALCKNIRDNTDVLSD 84

Qy 62 EFLVSDCNVTSRCKYKLKSTNTFCVTCENQAPVHFVGVGHC 104
Db 85 AFLPQCDRIKLPCHYKLLKSSNTICITCVNQLPIHFAGVGC 127

RESULT 7
Q98SM0 PRELIMINARY; PRT; 133 AA.
ID Q98SM0
AC Q98SM0;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351209; AAK30255.1; -.
DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;

Query Match 50.8%; Score 293; DB 13; Length 133;
Best Local Similarity 49.1%; Pred. No. 5e-26;
Matches 54; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

Qy 2 DMLTFQKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKN 57
Db 24 NWATFQKKHLTNTSINCNTINDNNIYVGGCKGVNTFISSATVKAICTGVI-MNV 82
Qy 58 LTTSEFYISDC---NVTSRPCKYKLKSTNTFCVTCENQAPVHFVGVGHC 104
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```
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RA Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242556; AAG31442.2; -.
DR HSSP; P22069; 10NC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 128 AA; 14804 MW; AFE6FD67D266C7C2 CRC64;

Query Match 52.7%; Score 304; DB 13; Length 128;
Best Local Similarity 53.4%; Pred. No. 2.6e-27;
Matches 55; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

Qy 2 DMLTFQKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLTS 61
Db 25 DWETFQKKHLTDTRDKVCKDAEMKALFDCKKNTFIYALPGRVKALCKNIRDNTDVLSD 84

Qy 62 EFLVSDCNVTSRCKYKLKSTNTFCVTCENQAPVHFVGVGHC 104
Db 85 VFYLPQCNRRKKLPCHYRLDGTNTICLTCKELPIHFAGVGC 127

RESULT 7
Q98SM0 PRELIMINARY; PRT; 133 AA.
ID Q98SM0
AC Q98SM0;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351209; AAK30255.1; -.
DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;

Query Match 50.8%; Score 293; DB 13; Length 133;
Best Local Similarity 49.1%; Pred. No. 5e-26;
Matches 54; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

Qy 2 DMLTFQKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKN 57
Db 24 NWATFQKKHLTNTSINCNTINDNNIYVGGCKGVNTFISSATVKAICTGVI-MNV 82
Qy 58 LTTSEFYISDC---NVTSRPCKYKLKSTNTFCVTCENQAPVHFVGVGHC 104
```





GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:10 ; Search time 29.5753 Seconds  
(without alignments)  
1109.503 Million cell updates/sec

Title: US-09-961-400-11  
Perfect score: 577  
Sequence: 1 SDWLTFQKXHLNTRDVCN.....TFCVTCENQAPVHFVGVGHC 104

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues  
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : SPTREMBL\_25:\*
- 1: sp\_archaea:\*
  - 2: sp\_bacteria:\*
  - 3: sp\_fungi:\*
  - 4: sp\_human:\*
  - 5: sp\_invertebrate:\*
  - 6: sp\_mammal:\*
  - 7: sp\_mhc:\*
  - 8: sp\_organelle:\*
  - 9: sp\_phase:\*
  - 10: sp\_plant:\*
  - 11: sp\_rodent:\*
  - 12: sp\_virus:\*
  - 13: sp\_vertebrate:\*
  - 14: sp\_unclassified:\*
  - 15: sp\_ivirus:\*
  - 16: sp\_bacteriap:\*
  - 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	573	99.3	127	13 Q8UVX5	Q8UVX5 rana pipien
2	551	95.5	127	13 Q8UVX5	Q8UVX5 rana pipien
3	399.5	69.2	129	13 Q8DFY6	Q8DFY6 rana catesb
4	381	66.0	128	13 Q8DFY8	Q8DFY8 rana catesb
5	306	53.0	128	13 Q8DFY7	Q8DFY7 rana catesb
6	304	52.7	128	13 Q8DFY5	Q8DFY5 rana catesb
7	293	50.8	133	13 Q8SFM0	Q8SFM0 rana catesb
8	281	48.7	132	13 Q8SFM2	Q8SFM2 rana catesb
9	281	48.7	133	13 Q8SL9	Q8SL9 rana catesb
10	277	48.0	133	13 Q8SL8	Q8SL8 rana catesb
11	275	47.7	132	13 Q8SM1	Q8SM1 rana catesb
12	270.5	46.9	132	13 Q8DF78	Q8DF78 rana catesb
13	157.5	27.3	169	13 Q9W738	Q9W738 xenopus lae
14	133	23.1	152	11 Q9JKI5	Q9JKI5 mus saxicol
15	131	22.7	157	11 Q9UK19	Q9UK19 meriones un
16	130.5	22.6	153	11 Q9JKI7	Q9JKI7 mus saxicol

17	130	22.5	157	11 Q9UKJ3	Q9UKJ3 meriones un
18	128.5	22.3	146	6 Q861V3	Q861V3 pygathrix r
19	128.5	22.3	146	6 Q861V2	Q861V2 pygathrix b
20	128.5	22.3	146	6 Q861V1	Q861V1 pygathrix a
21	127	22.0	154	11 Q9UKI8	Q9UKI8 mus saxicol
22	127	22.0	157	11 Q9UKJ4	Q9UKJ4 meriones un
23	126	21.8	157	11 Q9UKJ1	Q9UKJ1 meriones un
24	125	21.7	157	11 Q9UKJ2	Q861V4 trachypithe
25	124.5	21.6	146	6 Q861V4	Q9JKH9 mus pahari
26	124.5	21.6	155	11 Q9UKH9	Q9JKH9 mus pahari
27	123.5	21.4	155	11 Q9UKI3	Q9JKI3 mus saxicol
28	121	21.0	147	6 Q7YR36	Q7YR36 balaena mys
29	120.5	20.9	155	11 Q9UKI6	Q9UKI6 mus saxicol
30	119.5	20.7	155	11 Q9UKI2	Q9UKI2 mus saxicol
31	119.5	20.7	155	11 Q9UKI4	Q9UKI4 mus saxicol
32	118	20.5	147	6 Q7YR35	Q7YR35 tursiops tr
33	117.5	20.4	155	11 Q9UKI34	Q9UKI34 rattus norv
34	117	20.3	156	11 Q9UKG6	Q9UKG6 mus caroli
35	117	20.3	156	11 Q9UKH7	Q9UKH7 mus caroli
36	116.5	20.2	132	6 Q9TV25	Q9TV25 eulemur ful
37	116.5	20.2	155	11 Q9UKI25	Q9UKI25 mus musculu
38	116.5	20.2	155	11 Q9UKH8	Q9UKH8 mus pahari
39	116	20.1	156	11 Q9UKG7	Q9UKG7 mus caroli
40	115	19.9	146	6 Q861Y5	Q861Y5 colobus gue
41	115	19.9	156	11 Q9UKH4	Q9UKH4 mus caroli
42	115	19.9	156	11 Q9UKG9	Q9UKG9 mus caroli
43	115	19.9	156	11 Q9UKH5	Q9UKH5 mus caroli
44	114.5	19.8	132	6 Q9TV24	Q9TV24 galago moho
45	114.5	19.8	170	6 Q9BECL	Q9BECL tragulus ja

ALIGNMENTS

RESULT 1

Q918V8	PRELIMINARY;	PRT;	127 AA.
ID Q918V8			
AC Q918V8			
DT 01-OCT-2000	(TRENBLrel. 15, Created)		
DT 01-OCT-2000	(TRENBLrel. 15, Last sequence update)		
DT 01-OCT-2003	(TRENBLrel. 25, Last annotation update)		
DE	Onconase variant rapRL precursor.		
OS	Rana pipiens (Northern leopard frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.		
OX	NCBI_TaxID=8404;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Liver;		
RX	MEDLINE=20330357; PubMed=10871370;		
RA	Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;		
RT	"A gender-specific mRNA encoding a cytotoxic ribonuclease contains a		
RT	3' UTR of unusual length and structure."		
RL	Nucleic Acids Res. 28:2375-2382(2000).		
DR	EMBL; AF165133; AAF76935.1; -		
DR	PIR; A39035; A39035.		
DR	HSSB; P22069; LONC.		
DR	GO; GO:0003676; F:nucleic acid binding; IEA.		
DR	GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.		
DR	InterPro; IPR001427; RNaseA.		
DR	Pfam; PF00074; rnaseA; 1.		
DR	ProDom; PD000535; RNaseA; 1.		
DR	SMART; SM00092; RNase_Pc; 1.		
DR	PROSITE; PS00127; RNASE_PANCREATIC; 1.		
KW	SIGNAL.		
FT	SIGNAL		
SQ	SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;		

Query Match 99.3%; Score 573; DB 13; Length 127;  
Best Local Similarity 100.0%; Pred. No. 2e-58;  
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 DMLTFQKXHLNTRDVCNINMSTNLFHCKDKNTFYSRPEPKATCKGIIASKNVLTS 61



DR GO:0004522; F:pancreatic ribonuclease activity; IEA.  
DR InterPro: IPR001427; RNaseA.  
DR Pfam: PF00074; RNaseA; 1.  
DR ProDom: PD000535; RNaseA; 1.  
DR SMART: SM00092; RNase\_Pc; 1.  
DR PROSITE: PS00127; RNASE\_PANCREATIC; 1.  
KW SIGNAL.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 22 132 RC-RNASEL1 RIBONUCLEASE.  
SQ SEQUENCE 132 AA; 14625 MW; D8D9A517452FBE53 CRC64;  
Query Match 45.5%; Score 265.5; DB 13; Length 132;  
Best Local Similarity 43.2%; Pred. No. 5.6e-23;  
Matches 48; Conservative 18; Mismatches 38; Indels 7; Gaps 2;  
QY 2 QDWLTFQKKHLNTRDVCNNILSTNLF---HCKDKNTFIYSRPEPVKAICKGIATSKN 57  
DB 22 QNWKAFKFKHITSTSIDCNTIMDKAIYIVGGCKKERNTFIISDNVKAICSGVSPDRK 81  
QY 58 VLTTFEFLSDC--NATSRPKYKLLKSTNTFCVTCENQAPVHFVGVC 105  
DB 82 ELSTTSFKLNTCIRDSITPRCPYHSPDNNKICVKCEKQLPVHFVGIGKC 132  
RESULT 13  
Q9W738 PRELIMINARY; PRT; 169 AA.  
ID Q9W738  
AC Q9W738; 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE FRL2 protein.  
GN FRL2.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.  
NCBI\_TaxID=8355;  
[1]  
EN NCBI\_TaxID=8355;  
RP SEQUENCE FROM N.A.  
RA MEDLINE=96069663; PubMed=7585965;  
RA Kinoshita N., Minshall J., Kirschner M.W.;  
RT "The identification of two novel ligands of the FGF receptor by a  
RT yeast screening method and their activity in Xenopus development.";  
RL Cell 83:621-630 (1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Kinoshita N., Kirschner M.W.;  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF159166; AAD41901.1; -.  
DR HSP: P06566; 1L5Q.  
DR GO:0003676; F:nucleic acid binding; IEA.  
DR GO:0004522; F:pancreatic ribonuclease activity; IEA.  
DR InterPro: IPR001427; RNaseA.  
DR Pfam: PF00074; RNaseA; 1.  
DR ProDom: PD000535; RNaseA; 1.  
DR PROSITE: PS00127; RNASE\_PANCREATIC; 1.  
SQ SEQUENCE 169 AA; 18831 MW; D969F3E43B3CE1B8 CRC64;  
Query Match 26.5%; Score 154.5; DB 13; Length 169;  
Best Local Similarity 36.1%; Pred. No. 5.7e-10;  
Matches 39; Conservative 18; Mismatches 36; Indels 15; Gaps 6;  
QY 7 FOKKHLNTRDVCN-----NILSTNLFHCKDKNTFIYSRPEPVKAICKGIATSKN 58  
DB 33 FMEKHIVKEGATNCNQTIKDRIKFN--NCKFNTFIHDTNGKKVKEMCAGIVKSTFV 90  
QY 59 LTTTFEFLSDC--NATSRP--CKYKLLKSTNTFCVTCENQAPVHFVG 101  
DB 91 ISKELLPLTDCLLMGRTAPPCNCAYNQTRTGTGTTTCNNYPPVHFAG 138  
RESULT 14

RESULT 11  
Q98SM1 PRELIMINARY; PRT; 132 AA.  
ID Q98SM1  
AC Q98SM1; 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE RNase A-type ribonuclease rc204 precursor.  
OS Rana catesbeiana (Bull frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.  
NCBI\_TaxID=8400;  
[1]  
EN NCBI\_TaxID=8400;  
RP SEQUENCE FROM N.A.  
RA MEDLINE=21539506; PubMed=11683320;  
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;  
RT "rapid diversification of RNase A superfamily ribonuclease from the  
RT bullfrog, Rana catesbeiana."  
RL J. Mol. Evol. 53:31-38 (2001).  
DR EMBL: AF351208; AAK30254.1; -.  
DR HSP: P11916; 1BC4.  
DR GO:0003676; F:nucleic acid binding; IEA.  
DR GO:0004522; F:pancreatic ribonuclease activity; IEA.  
DR InterPro: IPR001427; RNaseA.  
DR Pfam: PF00074; RNaseA; 1.  
DR ProDom: PD000535; RNaseA; 1.  
DR SMART: SM00092; RNase\_Pc; 1.  
DR PROSITE: PS00127; RNASE\_PANCREATIC; 1.  
KW SIGNAL.  
FT SIGNAL 1 22 POTENTIAL.  
FT CHAIN 132 AA; 14704 MW; 95D61760F729868E CRC64;  
SQ SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;  
Query Match 46.2%; Score 270; DB 13; Length 132;  
Best Local Similarity 47.7%; Pred. No. 1.7e-23;  
Matches 53; Conservative 13; Mismatches 37; Indels 8; Gaps 3;  
QY 2 QDWLTFQKKHLNTRDVCNNILSTNLF---HCKDKNTFIYSRPEPVKAICKGIATSKN 57  
DB 23 QDNFTQKKHITSTSIDCNTIMDKIYIVGGCKKVNFTIYSATTVKAICTGVLSN-N 81  
QY 58 VLTTFEFLSDC--NATSRPKYKLLKSTNTFCVTCENQAPVHFVGVC 105  
DB 82 VLSTTRFQLXXXTRFTITSRCPYSSYKTKIKVCKENEPVHFAGIGKC 132  
RESULT 12  
Q9DF78 PRELIMINARY; PRT; 132 AA.  
ID Q9DF78  
AC Q9DF78; 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE RC-RNaseL1 ribonuclease precursor.  
OS Rana catesbeiana (Bull frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.  
NCBI\_TaxID=8400;  
[1]  
EN NCBI\_TaxID=8400;  
RP SEQUENCE FROM N.A.  
RA TISSUE=Liver;  
RA MEDLINE=20512555; PubMed=11058105;  
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;  
RT "Purification and cloning of cytotoxic ribonucleases from Rana  
RT catesbeiana (bullfrog)."  
RL Nucleic Acids Res. 28:4097-4104 (2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA TISSUE=Liver;  
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF288642; AAG30414.2; -.  
DR HSP: P11916; 1BC4.  
DR GO:0003676; F:nucleic acid binding; IEA.

[illegible]

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Db 24 QNWTFQKKHLTDTRDVCKDAEMKALFDCKQKNTFIYRPGRVQALCKNIIVKSNVLT 83
QY 62 FEYILSDCNATSRPCKYKLLKSTNTFCVTENQAPVHFVGVGHC 105
Db 84 DEFYILSDCNRIKLPCHYKLLKSSNTTICITCENKPLVHFVAVEEC 127

RESULT 5
Q9DFY7
ID Q9DFY7 PRELIMINARY; PRT; 128 AA.
AC Q9DFY7;
DT 01-WAR-2001 (Tremblrel. 16, Created)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE RC-RNase3 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN SEQUENCE FROM N.A.
RP TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
DR EMBL; AF242554; AAG31440.2; -.
DR HSSP; P22069; IONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNase3 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;

Query Match 52.6%; Score 307; DB 13; Length 128;
Best Local Similarity 53.8%; Pred. No. 8.2e-28;
Matches 56; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

QY 2 QDWLTFQKKHLTDTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGLIASKNVLT 61
Db 24 QDWTFQKKHLTDTRDVCKDAEMKALFDCKQKNTFIYALPGRVQALCKNIRDNDVLSR 83

QY 62 FEYILSDCNATSRPCKYKLLKSTNTFCVTENQAPVHFVGVGHC 105
Db 84 DAFLLPQCDRIKLPCHYKLLKSSNTTICITCYNQLPIHFAGVGC 127

RESULT 6
Q9DFY5
ID Q9DFY5 PRELIMINARY; PRT; 128 AA.
AC Q9DFY5;
DT 01-WAR-2001 (Tremblrel. 16, Created)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE RC-RNase6 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN SEQUENCE FROM N.A.
RP TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
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RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242556; AAG31442.2; -.
DR HSSP; P22069; IONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNase6 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14804 MW; AFBFD67D266C7C2 CRC64;

Query Match 52.2%; Score 305; DB 13; Length 128;
Best Local Similarity 52.9%; Pred. No. 1.4e-27;
Matches 55; Conservative 14; Mismatches 35; Indels 0; Gaps 0;

QY 2 QDWLTFQKKHLTDTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGLIASKNVLT 61
Db 24 QDWLTFQKKHLTDTRDVCKDAEMKALFDCKQKNTFIYFARPRVQALCKNIKDNITVLSR 83

QY 62 FEYILSDCNATSRPCKYKLLKSTNTFCVTENQAPVHFVGVGHC 105
Db 84 DVFYLPQCNRRKLPCHYRLDGSNTTICLTCKMKELPIHFAGVGC 127

RESULT 7
Q98SM0
ID Q98SM0 PRELIMINARY; PRT; 133 AA.
AC Q98SM0;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351209; AAK30255.1; -.
DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00032; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;
SQ SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;

Query Match 50.0%; Score 292; DB 13; Length 133;
Best Local Similarity 49.5%; Pred. No. 4.7e-26;
Matches 55; Conservative 14; Mismatches 34; Indels 8; Gaps 3;

QY 2 QDWLTFQKKHLTDTRDVDCNNILSTNLF---HCKDKNTFIYSRPEPVKAICKGLIASKN 57
Db 23 QNWATFOQKHITNTSSINCNTIMDNITIVGQCKGVNTFISSATTVAICTGVI--NNN 81
QY 58 VLTTFEYILSDCNATSRPCKYKLLKSTNTFCVTENQAPVHFVGVGHC 105
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|||||
24 QDWLTFQKKHLNTRDVCNNILNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 83
62 FEFYLSDCNATSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
|||||
84 SEFYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 2
Q9DFY6
ID Q8UVX5 PRELIMINARY; PRT; 127 AA.
AC Q8UVX5
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE RC-RNase4 ribonuclease precursor.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Wang S.-C.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332139; AAL54383.1; -.
DR PIR; A39035; A39035.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 129 RC-RNase4 RIBONUCLEASE.
SQ SEQUENCE 127 AA; 14469 MW; 953F90D351CFEF3 CRC64;

Query Match 93.0%; Score 543; DB 13; Length 127;
Best Local Similarity 93.3%; Pred. No. 3.1e-55;
Matches 97; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 QDWLTFQKKHLNTRDVCNNILNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 61
Db 24 QDWLTFQKKHLNTRDVCNNILNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 83

QY 62 FEFYLSDCNATSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
Db 84 SEFYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 3
Q9DFY6
ID Q9DFY6 PRELIMINARY; PRT; 129 AA.
AC Q9DFY6
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE RC-RNase4 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242553; AAG31439.1; -.
DR PDB; 1M58; 09-JAN-03.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNase2 RIBONUCLEASE.
SQ SEQUENCE 129 AA; 14724 MW; 826A62882B10ABDA CRC64;

Query Match 65.4%; Score 382; DB 13; Length 128;
Best Local Similarity 66.3%; Pred. No. 1.6e-36;
Matches 69; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

QY 2 QDWLTFQKKHLNTRDVCNNILNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 61
Db 24 QDWLTFQKKHLNTRDVCNNILNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 83
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SEQUENCE FROM N.A.
TISSUE=Liver;
Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242555; AAG31441.2; -.
DR PDB; 1KVZ; 28-JUL-02.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 129 RC-RNase4 RIBONUCLEASE.
SQ SEQUENCE 129 AA; 14724 MW; 826A62882B10ABDA CRC64;

Query Match 67.0%; Score 391.5; DB 13; Length 129;
Best Local Similarity 64.8%; Pred. No. 1.3e-37;
Matches 68; Conservative 17; Mismatches 19; Indels 1; Gaps 1;

QY 2 QDWLTFQKKHLNTRDVCNNILNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 61
Db 24 QDWLTFQKKHLNTRDVCNNILNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 83

QY 62 FEFYLSDCNATSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
Db 84 SEFYLAECNVKPRKPKYKLLKSSNRICRCEHELPHVHFAGVGIC 128

RESULT 4
Q9DFY8
ID Q9DFY8 PRELIMINARY; PRT; 128 AA.
AC Q9DFY8
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE RC-RNase2 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104 (2000).
RN [2]
RP SEQUENCE FROM N.A.
TISSUE=Liver;
Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242553; AAG31439.1; -.
DR PDB; 1M58; 09-JAN-03.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNase2 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14839 MW; 989719CF52053ECC CRC64;

Query Match 65.4%; Score 382; DB 13; Length 128;
Best Local Similarity 66.3%; Pred. No. 1.6e-36;
Matches 69; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

QY 2 QDWLTFQKKHLNTRDVCNNILNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 61
Db 24 QDWLTFQKKHLNTRDVCNNILNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 83
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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:10 ; Search time 29.8597 seconds  
(without alignments)  
1109.503 Million cell updates/sec

Title: US-09-961-400-8

Perfect score: 584

Sequence: 1 MQDWLTFQKKHLTNTRDVC.....TFCVTCENQAPVHFVGVGHC 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL\_25.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	565	96.7	127	13	Q918V8
2	543	93.0	127	13	Q8UUV5
3	391.5	67.0	129	13	Q9DFV6
4	382	65.4	128	13	Q9DFY8
5	307	52.6	128	13	Q9DFY7
6	305	52.2	128	13	Q9DFV5
7	292	50.0	133	13	Q98SM0
8	279	47.8	132	13	Q98SM2
9	276	47.3	133	13	Q98SL9
10	272	46.6	133	13	Q98SL8
11	270	46.2	132	13	Q98SM1
12	265.5	45.5	132	13	Q9DF78
13	154.5	26.5	169	13	Q9W738
14	120	20.5	157	11	Q9JKJ3
15	120	20.5	157	11	Q9JKI9
16	119.5	20.5	146	6	Q86LY3

17	119.5	20.5	146	6	Q86LY2
18	119.5	20.5	146	6	Q86LY1
19	118	20.2	157	11	Q9JKJ4
20	117	20.0	157	11	Q9JKJ2
21	116	19.9	152	11	Q9JKI5
22	115.5	19.8	153	11	Q9JKI7
23	115	19.7	147	6	Q7YRJ5
24	115	19.7	157	11	Q9JKJ1
25	114.5	19.6	146	6	Q86LY4
26	113.5	19.4	132	6	Q9TV24
27	113	19.3	147	6	Q7YRJ6
28	111.5	19.1	119	6	Q9TSQ6
29	111.5	19.1	119	6	Q9TV32
30	111.5	19.1	147	6	Q8HZQ0
31	110.5	18.9	119	6	Q9TV30
32	110	18.8	154	11	Q9JKI8
33	109.5	18.8	155	11	Q9JKH9
34	108.5	18.6	132	6	Q9TV25
35	108.5	18.6	155	11	Q9JKI3
36	108	18.5	124	6	Q95NE6
37	108	18.5	146	6	Q86LY5
38	106.5	18.2	155	11	Q9JKH8
39	106.5	18.2	170	6	Q9BEC1
40	106	18.2	144	6	Q9BH14
41	105.5	18.1	144	11	Q8OZ85
42	105.5	18.1	153	11	Q8OXS4
43	105.5	18.1	155	11	Q9JKI6
44	104.5	17.9	119	6	Q9TV31
45	104.5	17.9	155	11	Q9JKI2

#### ALIGNMENTS

RESULT 1

ID Q918V8 PRELIMINARY; PRT; 127 AA.  
AC Q918V8;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Onconase variant rap1 precursor  
OS Rana pipiens (Northern leopard frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
OX NCBI\_TaxID=8404;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
EX MEDLINE=20330357; PubMed=10871370;  
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;  
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a  
RT 3' UTR of unusual length and structure."  
RL Nucleic Acids Res. 28:2375-2382(2000).  
DR EMBL; AF165133; AAF76935.1; -  
DR PIR; A39035; A39035.  
DR HSPF; P22069; IONC.  
DR GO; GO:0003676; F:nucleic acid binding; IEA.  
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.  
DR InterPro; IPR001427; RNaseA.  
DR Pfam; PF00074; rnaaseA; 1.  
DR ProDom; PD000535; rnaaseA; 1.  
DR SMART; SM00032; RNase\_Fc; 1.  
DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
KW SIGNAL.  
FT SIGNAL  
SQ SEQUENCE 1 23 POTENTIAL.  
SEQUENCE 127 AA; 14491 MW; B851DC5407AB69B CRC64;

Query Match 96.7%; Score 565; DB 13; Length 127;  
Best Local Similarity 97.1%; Pred. No. 8.7e-58;  
Matches 101; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 QDWLTFQKKHLTNTRDVCNNILSTNLPHCKDKNTFYSRPEPKAICKGLIASKNVLT 61



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Q861Y3
ID Q861Y3 PRELIMINARY; PRT; 146 AA.
AC Q861Y3;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Angiogenin.
OS Pygathrix roxellana (golden snub-nosed monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=61622;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22597544; PubMed=12711394;
RA Zhang J., Zhang Y.-P.;
RT "Pseudogenization of the tumor-growth promoter angiogenin in a leaf-
RT eating monkey.";
RL Gene 308:95-101(2003).
DR EMBL; AY221130; AAC41337.1; -.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SEQUENCE 146 AA; 16438 MW; 8CF170A4BD12BA67 CRC64;

Query Match 22.2%; Score 129.5; DB 6; Length 146;
Best Local Similarity 34.2%; Pred. No. 4.2e-07;
Matches 38; Conservative 16; Mismatches 40; Indels 17; Gaps 7;

QY 2 QDWLTFOKKHLTNT----RDVDCNNIMSTN--LFHCKDKNTFIYSRPEPVKAIC---KGI 52
DB 31 RDFLT---KHYDATPQGRNDRYCESMRRRGITSPCKDINTFIHGNRSRHIKAICGDENG 87
QY 53 IASKNV-LTTSEFYLSDCNV---TSR-PCKYKLLKSTNTFCVTCENQAPVH 98
DB 88 PYGENLRISKSPFQVTTCTNLRGSSRPPCRATAGFRNIVVACENDLPVH 138

RESULT 15
Q861Y2
ID Q861Y2 PRELIMINARY; PRT; 146 AA.
AC Q861Y2;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Angiogenin.
OS Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=61621;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22597544; PubMed=12711394;
RA Zhang J., Zhang Y.-P.;
RT "Pseudogenization of the tumor-growth promoter angiogenin in a leaf-
RT eating monkey.";
RL Gene 308:95-101(2003).
DR EMBL; AY221131; AAC41338.1; -.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SEQUENCE 146 AA; 16438 MW; 8CF170A4BD12BA67 CRC64;

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Query Match 22.2%; Score 129.5; DB 6; Length 146;
Best Local Similarity 34.2%; Pred. No. 4.2e-07;
Matches 38; Conservative 16; Mismatches 40; Indels 17; Gaps 7;

QY 2 QDWLTFOKKHLTNT----RDVDCNNIMSTN--LFHCKDKNTFIYSRPEPVKAIC---KGI 52
DB 31 RDFLT---KHYDATPQGRNDRYCESMRRRGITSPCKDINTFIHGNRSRHIKAICGDENG 87
QY 53 IASKNV-LTTSEFYLSDCNV---TSR-PCKYKLLKSTNTFCVTCENQAPVH 98
DB 88 PYGENLRISKSPFQVTTCTNLRGSSRPPCRATAGFRNIVVACENDLPVH 138

Search completed: May 7, 2004, 21:46:01
Job time : 29.8597 secs

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## RESULT 11

Q98SM1 ID Q98SM1 PRELIMINARY; PRT; 132 AA.  
 AC Q98SM1;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE RNase A-type ribonuclease rc204 precursor.  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21539506; PubMed=11683320;  
 RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;  
 RT "Rapid diversification of RNase A superfamily ribonuclease from the  
 RT bullfrog, *Rana catesbeiana*.";  
 RL J. Mol. Evol. 53:31-38 (2001).  
 DR EMBL; AF351208; AAK30254.1; -.  
 DR HSP; P11916; 1BC4.  
 DR GO; GO:0003676; F:nucleic acid binding; IEA.  
 DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.  
 DR InterPro; IPR001427; RNaseA.  
 DR Pfam; PF00074; rnasea; 1.  
 DR ProDom; PD000535; RNaseA; 1.  
 DR SMART; SM00092; RNase PC; 1.  
 DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
 KW SIGNAL.  
 FT SIGNAL.  
 SQ SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;

Query Match 48.0%; Score 280; DB 13; Length 132;  
 Best Local Similarity 48.6%; Pred. No. 1.4e-24;  
 Matches 54; Conservative 14; Mismatches 35; Indels 8; Gaps 3;  
 QY 2 QDWLTFQKHLNTRDVCNNIMSNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 57  
 Db 23 QDWPTFQKHPTSSIDCNTIMDKDIYIVRGCKKVNFTFIYSATTVKACITGVLSN-N 81  
 QY 58 VLTTSFYLSDCN---VTSRPCKYKLKSTNTFCVTCNQAPVHFVGHC 105  
 Db 82 VLSTTRFQLXXXTRFTIYSRPEPVKAICKGIASKN 132

## RESULT 12

Q9DF78 ID Q9DF78 PRELIMINARY; PRT; 132 AA.  
 AC Q9DF78;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE RC-RNaseL1 ribonuclease precursor.  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=Liver;  
 RX MEDLINE=20512555; PubMed=11058105;  
 RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;  
 RT "Purification and cloning of cytotoxic ribonucleases from *Rana*  
 RT catesbeiana (bullfrog).";  
 RL Nucleic Acids Res. 28:4097-4104 (2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF288642; AAG30414.2; -.  
 DR HSP; P11916; 1BC4.  
 DR GO; GO:0003676; F:nucleic acid binding; IEA.

DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.  
 DR InterPro; IPR001427; RNaseA.  
 DR Pfam; PF00074; rnasea; 1.  
 DR ProDom; PD000535; RNaseA; 1.  
 DR SMART; SM00092; RNase PC; 1.  
 DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
 KW SIGNAL.  
 FT SIGNAL.  
 SQ SEQUENCE 132 AA; 14695 MW; D8D9A517452FBE53 CRC64;

Query Match 47.3%; Score 275.5; DB 13; Length 132;  
 Best Local Similarity 44.1%; Pred. No. 4.6e-24;  
 Matches 49; Conservative 19; Mismatches 36; Indels 7; Gaps 2;  
 QY 2 QDWLTFQKHLNTRDVCNNIMSNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 57  
 Db 22 QWAXFKEKHITSSIDCNTIMDKAIYIVGCKKERNTFIISSEDNVKAICGVSPPDK 81  
 QY 58 VLTTSFYLSDC---NVTSPCKYKLKSTNTFCVTCNQAPVHFVGHC 105  
 Db 82 ELSTTSFKLNTCIRDSITPRPCYHPSPDNNKICVACEKQLPVPVFGKGC 132

## RESULT 13

Q9W738 ID Q9W738 PRELIMINARY; PRT; 169 AA.  
 AC Q9W738;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE FRL2 protein.  
 GN FRL2.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96069863; PubMed=7585965;  
 RA Kinoshita N., Minshull J., Kirschner M.W.;  
 RT "The identification of two novel ligands of the FGF receptor by a  
 RT yeast screening method and their activity in *Xenopus* development.";  
 RL Cell 83:621-630 (1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Kinoshita N., Kirschner M.W.;  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF159166; AAD41901.1; -.  
 DR HSP; P00656; 1LSQ.  
 DR GO; GO:0003676; F:nucleic acid binding; IEA.  
 DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.  
 DR InterPro; IPR001427; RNaseA.  
 DR Pfam; PF00074; rnasea; 1.  
 DR ProDom; PD000535; RNaseA; 1.  
 DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
 SQ SEQUENCE 169 AA; 18891 MW; D969F3E43B3CE1B8 CRC64;

Query Match 27.0%; Score 157.5; DB 13; Length 169;  
 Best Local Similarity 36.1%; Pred. No. 2.8e-10;  
 Matches 39; Conservative 19; Mismatches 35; Indels 15; Gaps 6;  
 QY 7 FQKHLNTRDVCN-----NIMSTNLFCKCKNTFIYSRPEPVKAICKGIASKN 58  
 Db 33 FMEKHIVKEGAETNCNQTKDKRNFKN--NCKFNTFIHDTNGKVKEMCAGIVKSTFV 90  
 QY 59 LTTSEFYLSDCNV---TSRP--CKYKLKSTNTFCVTCNQAPVHFVG 101  
 Db 91 ISKELLPLTDLGMRTARFPNCAYNQTRTTGVNITCENNYVPHFAG 138

## RESULT 14



Db 24 QNWETFOKKHLTDRDVKCAEMKALFDCKQKNTFIYALPGRVQALCKNIIVSKNVLST 83  
 QY 62 SEFYSDCNVTSRPPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105  
 Db 84 DEFYSDCNRIKLPCHYKLLKSSNTICITCENKLPVHFVAVBEC 127

## RESULT 5

Q9DFV7  
 ID Q9DFY7 PRELIMINARY; PRT; 128 AA.  
 AC Q9DFY7  
 DT 01-MAR-2001 (TREMELrel. 16, Created)  
 DT 01-OCT-2001 (TREMELrel. 18, Last sequence update)  
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
 DE RC-RNase3 ribonuclease precursor.  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=20512555; PubMed=11058105;  
 RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;  
 RT "Purification and cloning of cytotoxic ribonucleases from Rana  
 catesbeiana (bullfrog).";  
 RL Nucleic Acids Res. 28:4097-4104(2000).  
 DR EMBL; AF242554; AAG31440.2; -;  
 DR HSSP; P22069; 10NC.  
 DR GO; GO:0003676; F:nucleic acid binding; IEA.  
 DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.  
 DR InterPro; IPR001427; RNaseA.  
 DR Pfam; PF00074; RNaseA.  
 DR ProDom; PD000535; RNaseA; 1.  
 DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
 KW SIGNAL.  
 FT CHAIN 1 23 POTENTIAL.  
 FT CHAIN 24 128 RC-RNase3 RIBONUCLEASE.  
 SQ SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;

Query Match 53.3%; Score 311; DB 13; Length 128;  
 Best Local Similarity 54.8%; Pred. No. 3.5e-28;  
 Matches 57; Conservative 12; Mismatches 35; Indels 0; Gaps 0;  
 QY 2 QDWLTFQKKHLTNTDRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLTT 61  
 Db 24 QNWETFOKKHLTDRDVKCDVEMAKALFDCKTNTFIYALPGRVQALCKNIRDNDVLSR 83  
 QY 62 SEFYSDCNVTSRPPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105  
 Db 84 DAFLPQCDRIKLPCHYKLLSSNTICITCVNQLPIHFAGVGC 127

## RESULT 6

Q9DFY5  
 ID Q9DFY5 PRELIMINARY; PRT; 128 AA.  
 AC Q9DFY5  
 DT 01-MAR-2001 (TREMELrel. 16, Created)  
 DT 01-OCT-2001 (TREMELrel. 18, Last sequence update)  
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
 DE RC-RNase6 ribonuclease precursor.  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=20512555; PubMed=11058105;  
 RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;  
 RT "Purification and cloning of cytotoxic ribonucleases from Rana  
 catesbeiana (bullfrog).";

RL Nucleic Acids Res. 28:4097-4104(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF242556; AAG31442.2; -;  
 DR HSSP; P22069; 10NC.  
 DR GO; GO:0003676; F:nucleic acid binding; IEA.  
 DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.  
 DR InterPro; IPR001427; RNaseA.  
 DR Pfam; PF00074; RNaseA; 1.  
 DR ProDom; PD000535; RNaseA; 1.  
 DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
 KW SIGNAL.  
 FT CHAIN 1 23 POTENTIAL.  
 FT CHAIN 24 128 RC-RNase6 RIBONUCLEASE.  
 SQ SEQUENCE 128 AA; 14804 MW; AFE6FD67D266C7C2 CRC64;  
 Query Match 53.0%; Score 309; DB 13; Length 128;  
 Best Local Similarity 53.8%; Pred. No. 5.9e-28;  
 Matches 56; Conservative 13; Mismatches 35; Indels 0; Gaps 0;  
 QY 2 QDWLTFQKKHLTNTDRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLTT 61  
 Db 24 QDWLTFQKKHLTDRDVKCDVEMKALFDCKTNTFIYALPGRVQALCKNIRDNDVLSR 83  
 QY 62 SEFYSDCNVTSRPPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105  
 Db 84 DVFYLPQCNRRKKLPCHYRLDGSNTICITCMKELPIHFAGVGC 127

## RESULT 7

Q98SMO  
 ID Q98SMO PRELIMINARY; PRT; 133 AA.  
 AC Q98SMO  
 DT 01-JUN-2001 (TREMELrel. 17, Created)  
 DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
 DE RNase A-type ribonuclease rc208 precursor.  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21539506; PubMed=11683320;  
 RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;  
 RT "Rapid diversification of RNase A superfamily ribonuclease from the  
 bullfrog, Rana catesbeiana";  
 RL J. Mol. Evol. 53:31-38(2001).  
 DR EMBL; AF351209; AAK30255.1; -;  
 DR HSSP; P11916; 1BC4.  
 DR GO; GO:0003676; F:nucleic acid binding; IEA.  
 DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.  
 DR InterPro; IPR001427; RNaseA.  
 DR Pfam; PF00074; RNaseA; 1.  
 DR ProDom; PD000535; RNaseA; 1.  
 DR SMART; SM00092; RNase\_PC; 1.  
 DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
 KW SIGNAL.  
 FT CHAIN 1 22 POTENTIAL.  
 SQ SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;  
 Query Match 51.1%; Score 298; DB 13; Length 133;  
 Best Local Similarity 49.5%; Pred. No. 1.2e-26;  
 Matches 55; Conservative 16; Mismatches 32; Indels 8; Gaps 3;  
 QY 2 QDWLTFQKKHLTNTDRDVCNNIMSTNLF----HCKDKNTFIYSRPPVKAICKGIIASKN 57  
 Db 23 QNWATFOKKHLTNTSSINCNTIMDNNTIYVGGQCKGVNTFISSATTCAICTGVI--NMN 81  
 QY 58 VLTITSEFYLSDC--NVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105

```

Db 24 QDWLTFQKKHLTNTDRVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 83
QY 62 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
Db 84 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 2
Q8UVX5 PRELIMINARY; PRT; 127 AA.
AC Q8UVX5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Onconase precursor.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Wang S.-C.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332139; AAL54383.1; -.
DR PIR; A39035; A39035.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 129 RC-RNASE4 RIBONUCLEASE.
SQ SEQUENCE 127 AA; 14469 MW; 953F90D351CPEEF3 CRC64;

Query Match 95.4%; Score 556; DB 13; Length 127;
Best Local Similarity 96.2%; Pred. No. 1.4e-56;
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 QDWLTFQKKHLTNTDRVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61
Db 24 QDWLTFQKKHLTNTDRVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 83
QY 62 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
Db 84 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 3
Q9DFY6 PRELIMINARY; PRT; 129 AA.
AC Q9DFY6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RC-RNase4 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242553; AAG31439.1; -.
DR PDB; 1M58; 09-JAN-03.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNASE2 RIBONUCLEASE.
SQ SEQUENCE 129 AA; 14724 MW; 826AG2892B10ABDA CRC64;

Query Match 66.2%; Score 386; DB 13; Length 128;
Best Local Similarity 67.3%; Pred. No. 7.1e-37;
Matches 70; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

QY 2 QDWLTFQKKHLTNTDRVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61

```

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RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242553; AAG31441.2; -.
DR PDB; 1KVZ; 28-JUL-02.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 129 RC-RNASE4 RIBONUCLEASE.
SQ SEQUENCE 129 AA; 14724 MW; 826AG2892B10ABDA CRC64;

Query Match 69.4%; Score 404.5; DB 13; Length 129;
Best Local Similarity 67.6%; Pred. No. 5.1e-39;
Matches 71; Conservative 16; Mismatches 17; Indels 1; Gaps 1;

QY 2 QDWLTFQKKHLTNTDRVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61
Db 24 QDWLTFQKKHLTNTDRVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 83
QY 62 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
Db 84 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 128

RESULT 4
Q9DFY8 PRELIMINARY; PRT; 128 AA.
AC Q9DFY8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RC-RNase2 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242553; AAG31439.1; -.
DR PDB; 1M58; 09-JAN-03.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNASE2 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14839 MW; 989719CF52053ECC CRC64;

Query Match 66.2%; Score 386; DB 13; Length 128;
Best Local Similarity 67.3%; Pred. No. 7.1e-37;
Matches 70; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

QY 2 QDWLTFQKKHLTNTDRVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61

```

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:10 ; Search time 29.8597 Seconds  
(without alignments)  
1109.503 Million cell updates/sec

Title: US-09-961-400-6  
Perfect score: 583  
Sequence: 1 MODWLTFOKKHLTNRDVC.....TFCVTCENQAPVHFVGVGHC 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:.\*  
1: sp\_archaea:.\*  
2: sp\_bacteria:.\*  
3: sp\_fungi:.\*  
4: sp\_human:.\*  
5: sp\_invertebrate:.\*  
6: sp\_mammal:.\*  
7: sp\_mhc:.\*  
8: sp\_organelle:.\*  
9: sp\_phase:.\*  
10: sp\_plant:.\*  
11: sp\_rodent:.\*  
12: sp\_virus:.\*  
13: sp\_vertebrate:.\*  
14: sp\_unclassified:.\*  
15: sp\_rvirus:.\*  
16: sp\_bacteriap:.\*  
17: sp\_archaeap:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	578	99.1	127	13	Q9i8v8 rana pipien
2	556	95.4	127	13	Q8uvx5 rana pipien
3	404.5	69.4	129	13	Q9DFY6 rana catesb
4	386	66.2	128	13	Q9dfy8 rana catesb
5	311	53.3	128	13	Q9DFY7 rana catesb
6	309	53.0	128	13	Q9dfy5 rana catesb
7	298	51.1	133	13	Q98SM0 rana catesb
8	286	49.1	133	13	Q98SL9 rana catesb
9	285	48.9	132	13	Q98SM2 rana catesb
10	282	48.4	133	13	Q98SL8 rana catesb
11	280	48.0	132	13	Q98SM1 rana catesb
12	275.5	47.3	132	13	Q9DF78 rana catesb
13	157.5	27.0	169	13	Q9W738 xenopus lae
14	129.5	22.2	146	6	Q861Y3 pygathrix a
15	129.5	22.2	146	6	Q861Y2 pygathrix b
16	129.5	22.2	146	6	Q861Y1 pygathrix a

17	129	22.1	152	11	Q9JKI5	Q9jki5 mus saxicol
18	127	21.8	157	11	Q9UKI9	Q9jki9 meriones un
19	126.5	21.7	153	11	Q9UKI7	Q9jki7 mus saxicol
20	126	21.6	157	11	Q9UKJ3	Q9jki3 meriones un
21	125.5	21.5	146	6	Q861Y4	Q861y4 trachypithe
22	125	21.4	157	11	Q9UKJ4	Q9jki4 meriones un
23	123	21.1	154	11	Q9UKI8	Q9jki8 mus saxicol
24	122	20.9	157	11	Q9UKJ1	Q9jki1 meriones un
25	121	20.8	147	6	Q7YRJ6	Q7yrj6 balaena mys
26	121	20.7	157	11	Q9UKJ2	Q9jki2 meriones un
27	120.5	20.7	155	11	Q9UKH9	Q9jkh9 mus pahari
28	119.5	20.5	155	11	Q9UKI3	Q9jki3 mus saxicol
29	118	20.2	147	6	Q7YRJ5	Q7yrj5 tursiops tr
30	116.5	20.0	155	11	Q9UKI6	Q9jki6 mus saxicol
31	115.5	19.8	132	6	Q9TV25	Q9tv25 eulemur ful
32	115.5	19.8	155	11	Q9UKI2	Q9jki2 mus saxicol
33	115.5	19.8	155	11	Q9UKI4	Q9jki4 mus saxicol
34	115	19.7	146	6	Q861Y5	Q861y5 colobus gue
35	114.5	19.6	132	6	Q9TV24	Q9tv24 galago moho
36	114.5	19.6	170	6	Q9BEC1	Q9bec1 tragulus ja
37	113.5	19.5	119	6	Q9TSQ6	Q9tsq6 cercopithec
38	113.5	19.5	119	6	Q9TV32	Q9tv32 gorilla gor
39	113.5	19.5	147	6	Q8HZQ0	Q8hzq0 pan troglod
40	113.5	19.5	155	11	Q9RL34	Q9rl34 rattus norv
41	113	19.4	156	11	Q9JKG6	Q9jkg6 mus caroli
42	113	19.4	156	11	Q9JKH7	Q9jkh7 mus caroli
43	112.5	19.3	119	6	Q9TV30	Q9tv30 saquinus oe
44	112.5	19.3	155	11	Q9RL25	Q9rl25 mus muscullu
45	112.5	19.3	155	11	Q9JKH8	Q9jkh8 mus pahari

## ALIGNMENTS

### RESULT 1

Q9i8v8 PRELIMINARY; PRT; 127 AA.  
AC Q9i8v8;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Onconase variant rapLR1 precursor.  
OS Rana pipiens (Northern leopard frog).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
OX NCBI\_TaxID=8404;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=20330357; PubMed=10871370;  
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;  
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a  
3' UTR of unusual length and structure.";  
RL Nucleic Acids Res. 28:2375-2382(2000).  
DR EMBL; AF165113; AAF76935.1; --  
DR PIR; A39035; A39035.  
DR HSP; P22069; IONC.  
DR GO; GO:0003676; F:nucleic acid binding; IEA.  
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.  
DR InterPro; IPR001427; RNaseA.  
DR Pfam; PF00074; RNaseA; 1.  
DR ProDom; PD000535; RNaseA; 1.  
DR SMART; SM00092; RNase\_Pc; 1.  
DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
KW Signal.  
FT SIGNAL  
SQ SEQUENCE 1 23 POTENTIAL.  
14491 MW; B8511DC5407AB69B CRC64;

Query Match 99.1%; Score 578; DB 13; Length 127;  
Best Local Similarity 100.0%; Pred. No. 4e-59;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QDWLTFQKKHLTNRDVCNNINSTNLFHCKDKNTFYSPPEVKAICKGIASKNVLT 61









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Db 24 QNWTFQKKHLTDRVDCDAEMKALFDCKQNTFIYARPGRVQALCKNIIVSKNVLST 83
QY 61 PEFYSDCNVTSRCPCKYKXKSTNTFCVTCENQAPVHFVGVGHC 104
Db 84 DEFYSDCNRIKLPCHYKXKSSNTICITCENKLPVHFVAVBEC 127

RESULT 5
Q9DFV7
ID Q9DFV7 PRELIMINARY; PRT; 128 AA.
AC Q9DFV7;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE RC-RNase3 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
DR EMBL; AF242554; AAG31440.2; -.
DR HSSP; P22069; 10NC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNase3 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;

Query Match 52.7%; Score 305; DB 13; Length 128;
Best Local Similarity 53.8%; Pred. No. 1.8e-27;
Matches 56; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

QY 1 QDWLTFQKKHLTDRVDCNNILTNLFCHCKDKNTFIYSRPEVPKAIKGLIASKNVLTT 60
Db 24 QDWTFQKKHLTDRVDCVEMAKALFDCKKNTFIYALPGRVKALCKNIRDNDVLSR 83
QY 61 PEFYSDCNVTSRCPCKYKXKSTNTFCVTCENQAPVHFVGVGHC 104
Db 84 DAFLLPQCDRIKLPCHYKXKSSNTICITCVNQLPIHFAGVGC 127

RESULT 6
Q9DFY5
ID Q9DFY5 PRELIMINARY; PRT; 128 AA.
AC Q9DFY5;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE RC-RNase6 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog).";

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RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242556; AAG31442.2; -.
DR HSSP; P22069; 10NC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNase6 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14804 MW; AFE6FD67D266C7C2 CRC64;

Query Match 52.3%; Score 303; DB 13; Length 128;
Best Local Similarity 52.9%; Pred. No. 3e-27;
Matches 55; Conservative 14; Mismatches 35; Indels 0; Gaps 0;

QY 1 QDWLTFQKKHLTDRVDCNNILTNLFCHCKDKNTFIYSRPEVPKAIKGLIASKNVLTT 60
Db 24 QDWLTFQKKHLTDRVDCVEMKALFDCKKNTFIYARPRVQALCKNIKNTINLSR 83
QY 61 PEFYSDCNVTSRCPCKYKXKSTNTFCVTCENQAPVHFVGVGHC 104
Db 84 DVFYLPQCNRRKKLPCHYRLDGSNTICITCMKELPIHFAGVGC 127

RESULT 7
Q98SMO
ID Q98SMO PRELIMINARY; PRT; 133 AA.
AC Q98SMO;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
bullfrog Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351209; AAK30255.1; -.
DR HSSP; P11916; 1RC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 133 AA; 14628 MW; 87FCF122C3499B02 CRC64;
SQ SEQUENCE 133 AA; 14628 MW; 87FCF122C3499B02 CRC64;

Query Match 50.4%; Score 292; DB 13; Length 133;
Best Local Similarity 48.6%; Pred. No. 5.9e-26;
Matches 54; Conservative 16; Mismatches 33; Indels 8; Gaps 3;

QY 1 QDWLTFQKKHLTDRVDCNNILTNLF-----HCKQKNTFIYSRPEVPKAIKGLIASKN 56
Db 23 QNATFQKKHLTDRVDCNNILTNLFIVGGQCKGVNTFIISATTVAICTGVI-NMN 81
QY 57 VLATTFEYLSDC--NVTSRPCKYKXKSTNTFCVTCENQAPVHFVGVGHC 104

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:10 ; Search time 29.5753 Seconds  
(without alignments)  
1109,503 Million cell updates/sec

Title: US-09-961-400-4  
Perfect score: 579  
Sequence: 1 QDWLTFQKKHLTNRDVCN.....TFCVTENQAPVHFVGVGHC 104

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL 25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	569	98.3	127	13	Q918V8	Q918V8 rana pipien
2	547	94.5	127	13	Q8UVX5	Q8UVX5 rana pipien
3	395.5	68.3	129	13	Q9DFV6	Q9DFV6 rana catesb
4	380	65.6	128	13	Q9DFY8	Q9DFY8 rana catesb
5	305	52.7	128	13	Q9DFY7	Q9DFY7 rana catesb
6	303	52.3	128	13	Q9DFY5	Q9DFY5 rana catesb
7	292	50.4	133	13	Q98SM0	Q98SM0 rana catesb
8	280	48.4	133	13	Q98SL9	Q98SL9 rana catesb
9	279	48.2	132	13	Q98SM2	Q98SM2 rana catesb
10	276	47.7	133	13	Q98SL8	Q98SL8 rana catesb
11	274	47.3	132	13	Q98SM1	Q98SM1 rana catesb
12	269.5	46.5	132	13	Q9DFV7	Q9DFV7 rana catesb
13	153.5	26.5	169	13	Q9W738	Q9W738 xenopus lae
14	122	21.1	157	11	Q9UKJ3	Q9UKJ3 meriones un
15	122	21.1	157	11	Q9UKI9	Q9UKI9 meriones un
16	120.5	20.8	146	6	Q86LY3	Q86LY3 pygathrix r

17	120.5	20.8	146	6	Q86LY2	Q86LY2 pygathrix b
18	120.5	20.8	146	6	Q86LY1	Q86LY1 pygathrix a
19	120	20.7	152	11	Q9UKI5	Q9UKI5 mus saxicol
20	120	20.7	157	11	Q9UKJ4	Q9UKJ4 meriones un
21	117.5	20.3	153	11	Q9UKI7	Q9UKI7 mus saxicol
22	117	20.2	157	11	Q9UKJ1	Q9UKJ1 meriones un
23	117	20.2	157	11	Q9UKJ2	Q9UKJ2 meriones un
24	116.5	20.1	146	6	Q86LY4	Q86LY4 trachypithe
25	114.5	19.8	132	6	Q9TV24	Q9TV24 galago moho
26	114	19.7	147	6	Q7VRJ5	Q7VRJ5 tursiops tr
27	114	19.7	154	11	Q9UKI8	Q9UKI8 mus saxicol
28	112	19.3	147	6	Q7VRJ6	Q7VRJ6 balaena mys
29	111.5	19.3	155	11	Q9UKH9	Q9UKH9 mus pahari
30	110.5	19.1	119	6	Q9TSQ6	Q9TSQ6 cercopithec
31	110.5	19.1	119	6	Q9TV32	Q9TV32 gorilla gor
32	110.5	19.1	132	6	Q9TV25	Q9TV25 eulemur ful
33	110.5	19.1	147	6	Q8HZQ0	Q8HZQ0 pan troglod
34	110.5	19.1	155	11	Q9UKI3	Q9UKI3 mus saxicol
35	109.5	18.9	119	6	Q9TV30	Q9TV30 saginus oe
36	109	18.8	146	6	Q86LY5	Q86LY5 colobus gue
37	108.5	18.7	155	11	Q9UKH8	Q9UKH8 mus pahari
38	108	18.7	156	11	Q923L6	Q923L6 mus musculu
39	107.5	18.6	155	11	Q9UKI6	Q9UKI6 mus saxicol
40	107	18.5	124	6	Q95NE6	Q95NE6 bubalus bub
41	106.5	18.4	155	11	Q9UKI2	Q9UKI2 mus saxicol
42	106.5	18.4	155	11	Q9RI34	Q9RI34 rattus norv
43	106.5	18.4	155	11	Q9UKI4	Q9UKI4 mus saxicol
44	105.5	18.2	144	11	Q80Z85	Q80Z85 mus musculu
45	105.5	18.2	153	11	Q80XS4	Q80XS4 mus musculu

#### ALIGNMENTS

RESULT 1

Q918V8 PRELIMINARY; PRT; 127 AA.  
ID Q918V8  
AC Q918V8;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Onconase variant rapLR1 precursor.  
OS Rana pipiens (Northern leopard frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
OX NCBI\_TaxID=8404;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=20330357; PubMed=10871370;  
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;  
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a  
3' UTR of unusual length and structure.";  
RL Nucleic Acids Res. 28:2375-2382(2000).  
DR EMBL; AF165133; AAF76935.1; -;  
DR PIR; A39035; A39035.  
DR HSP; P22069; IONC.  
DR GO; GO:0003676; F:nucleic acid binding; IEA.  
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.  
DR InterPro; IPR001427; RNaseA.  
DR Pfam; PF00074; rnaseA; 1.  
DR ProDom; PD000535; RNaseA; 1.  
DR SMART; SM00092; RNase\_Pc; 1.  
DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
KW SIGNAL.  
FT SIGNAL  
SQ SEQUENCE 1 23 POTENTIAL.  
14491 MW; B8511DC5407AB69B CRC64;  
Query Match 98.3%; Score 569; DB 13; Length 127;  
Best local similarity 98.1%; Pred. No. 4.7e-58;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QDWLTFQKKHLTNRDVCNLLSTNLFHCKDKNTFYSPFPVKAICKGLIASKNVLTT 60

Sat May 8 17:57:14 2004

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; ORGANISM: Rana pipiens
US-09-961-400-2
Query Match      46.8%; Score 281.5; DB 10; Length 104;
Best Local Similarity 49.5%; Pred. No. 2.9e-24;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

Qy 1 QNWATFOQKHIIINT-PIICNTIMDNIIYVGGQCKRYNTRFISSATTVKALCTGVI-NMN 58
Db 1 QDWLTFQKKHLTNTRDVCNNIMSTNLF----HCKDKNTFIYSRPEPVKALCKGIIASKN 56

Qy 59 VLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
Db 57 VLTISEEYVLSDC---NVTSRCKYKXKSTNTFCVTCENQAPVHFVGVGHC 104

Search completed: May 7, 2004, 21:51:57
Job time : 35.2947 secs
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; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with (His)6 tag, Met at
; OTHER INFORMATION: position 7, Met23Leu and Met58Leu substitutions
; OTHER INFORMATION: (recombinant Met(-1) RacOR1 Met22Leu Met57Leu-(His)6)
US-09-948-391A-22

Query Match          99.0%; Score 596; DB 10; Length 117;
Best Local Similarity 98.2%; Pred. No. 4.9e-60;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNWATFOQKHINTPIICNTIMDNNIYVGQCKRVNTFISSATTVKAICTGVINMNVL 60
Db 8 QNWATFOQKHINTPIICNTILDNNIYVGQCKRVNTFISSATTVKAICTGVINMNVL 67

Qy 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 68 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117

RESULT 13
US-09-961-400-22
; Sequence 22, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-22

Query Match          99.0%; Score 596; DB 10; Length 117;
Best Local Similarity 98.2%; Pred. No. 4.9e-60;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNWATFOQKHINTPIICNTIMDNNIYVGQCKRVNTFISSATTVKAICTGVINMNVL 60
Db 8 QNWATFOQKHINTPIICNTILDNNIYVGQCKRVNTFISSATTVKAICTGVINMNVL 67

Qy 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

```

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Db 68 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117

RESULT 14
US-09-948-391A-19
; Sequence 19, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: NEWTON, DIANNE L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met22Leu and
; OTHER INFORMATION: Met57Leu substitutions (recombinant RacOR1
; OTHER INFORMATION: Met22Leu Met57Leu)
US-09-948-391A-19

Query Match          98.0%; Score 590; DB 10; Length 110;
Best Local Similarity 97.3%; Pred. No. 2.2e-59;
Matches 107; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNWATFOQKHINTPIICNTIMDNNIYVGQCKRVNTFISSATTVKAICTGVINMNVL 60
Db 1 QNWATFOQKHINTPIICNTILDNNIYVGQCKRVNTFISSATTVKAICTGVINMNVL 60

Qy 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 15
US-09-961-400-2
; Sequence 2, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 104
; TYPE: PRT

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QY 61 STTRFQKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAITGVINMNVL 110  
 Db 61 STTRFQKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAITGVINMNVL 110

## RESULT 9

US-09-948-391A-17  
 ; Sequence 17, Application US/09948391A  
 ; Publication No. US20030027311A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rybak, Susanna M.  
 ; APPLICANT: The United States of America  
 ; APPLICANT: as represented by The Secretary of the  
 ; APPLICANT: Department of Health and Human Services  
 ; APPLICANT: Department of Health and Human Services  
 ; TITLE OF INVENTION: Recombinant Anti-Tumor RNase  
 ; FILE REFERENCE: 015280-343110US  
 ; CURRENT APPLICATION NUMBER: US/09/948,391A  
 ; CURRENT FILING DATE: 2002-05-10  
 ; PRIOR APPLICATION NUMBER: US 60/079,751  
 ; PRIOR FILING DATE: 1998-03-27  
 ; PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
 ; PRIOR FILING DATE: 1999-03-26  
 ; PRIOR APPLICATION NUMBER: US 09/622,613  
 ; PRIOR FILING DATE: 2000-08-17  
 ; NUMBER OF SEQ ID NOS: 43  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 17  
 ; LENGTH: 111  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:Rana  
 ; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1  
 ; OTHER INFORMATION: (recombinant Met (-1) RacOR1)  
 US-09-948-391A-17

Query Match 99.0%; Score 596; DB 10; Length 111;  
 Best Local Similarity 99.1%; Pred. No. 4.6e-60;  
 Matches 109; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNWATFQKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAITGVINMNVL 60  
 Db 2 QNWATFQKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAITGVINMNVL 61  
 QY 61 STTRFQKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAITGVINMNVL 110  
 Db 62 STTRFQKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAITGVINMNVL 111

## RESULT 10

US-09-948-391A-21  
 ; Sequence 21, Application US/09948391A  
 ; Publication No. US20030027311A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rybak, Susanna M.  
 ; APPLICANT: Newton, Dianne L.  
 ; APPLICANT: The United States of America  
 ; APPLICANT: as represented by The Secretary of the  
 ; APPLICANT: Department of Health and Human Services  
 ; APPLICANT: Department of Health and Human Services  
 ; TITLE OF INVENTION: Recombinant Anti-Tumor RNase  
 ; FILE REFERENCE: 015280-343110US  
 ; CURRENT APPLICATION NUMBER: US/09/948,391A  
 ; CURRENT FILING DATE: 2002-05-10  
 ; PRIOR APPLICATION NUMBER: US 60/079,751  
 ; PRIOR FILING DATE: 1998-03-27  
 ; PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
 ; PRIOR FILING DATE: 1999-03-26  
 ; PRIOR APPLICATION NUMBER: US 09/622,613  
 ; PRIOR FILING DATE: 2000-08-17  
 ; NUMBER OF SEQ ID NOS: 43  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 21

LENGTH: 111  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence:Rana  
 OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1,  
 OTHER INFORMATION: Met23Leu and Met58Leu substitutions (recombinant  
 OTHER INFORMATION: Met (-1) RacOR1 Met22Leu Met57Leu)  
 US-09-948-391A-21

Query Match 99.0%; Score 596; DB 10; Length 111;  
 Best Local Similarity 98.2%; Pred. No. 4.6e-60;  
 Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNWATFQKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAITGVINMNVL 60  
 Db 2 QNWATFQKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAITGVINMNVL 61  
 QY 61 STTRFQKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAITGVINMNVL 110  
 Db 62 STTRFQKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAITGVINMNVL 111

## RESULT 11

US-09-961-400-21  
 ; Sequence 21, Application US/09961400  
 ; Publication No. US20030124131A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: RYBAK, SUSANNA M.  
 ; APPLICANT: GOLDENBERG, DAVID M.  
 ; APPLICANT: NEWTON, DIANNE L.  
 ; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
 ; TITLE OF INVENTION: CELLS  
 ; FILE REFERENCE: 018733/1059  
 ; CURRENT APPLICATION NUMBER: US/09/961,400  
 ; CURRENT FILING DATE: 2001-09-25  
 ; PRIOR APPLICATION NUMBER: 09/622,613  
 ; PRIOR FILING DATE: 2000-08-17  
 ; PRIOR APPLICATION NUMBER: PCT/US99/06641  
 ; PRIOR FILING DATE: 1999-03-26  
 ; PRIOR APPLICATION NUMBER: 60/079,751  
 ; PRIOR FILING DATE: 1998-03-26  
 ; NUMBER OF SEQ ID NOS: 43  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 21  
 ; LENGTH: 111  
 ; TYPE: PRT  
 ; ORGANISM: Rana catesbeiana  
 US-09-961-400-21

Query Match 99.0%; Score 596; DB 10; Length 111;  
 Best Local Similarity 98.2%; Pred. No. 4.6e-60;  
 Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNWATFQKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAITGVINMNVL 60  
 Db 2 QNWATFQKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAITGVINMNVL 61  
 QY 61 STTRFQKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAITGVINMNVL 110  
 Db 62 STTRFQKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAITGVINMNVL 111

## RESULT 12

US-09-948-391A-22  
 ; Sequence 22, Application US/09948391A  
 ; Publication No. US20030027311A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rybak, Susanna M.  
 ; APPLICANT: Newton, Dianne L.  
 ; APPLICANT: The United States of America  
 ; APPLICANT: as represented by The Secretary of the  
 ; APPLICANT: Department of Health and Human Services

; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 60/079,751  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Rana catesbeiana  
US-09-961-400-24

Query Match  
Best Local Similarity 99.2%; Score 597; DB 10; Length 110;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWATFOQKHINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61  
DB 2 NWATFOQKHINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61  
QY 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRCP 110  
DB 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRCP 110

## RESULT 6

US-09-948-391A-26  
; Sequence 26, Application US/09948391A  
; Publication No. US20030027311A1  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: The United States of America  
; APPLICANT: as represented by the Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase  
; FILE REFERENCE: 015280-34311005  
; CURRENT APPLICATION NUMBER: US/09/948,391A  
; CURRENT FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: US 60/079,751  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: US 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 26  
; LENGTH: 111  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Rana  
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1  
; OTHER INFORMATION: and Gln2ser substitution (Met(-1) RacOR1 Q1S)  
US-09-948-391A-26

Query Match  
Best Local Similarity 99.2%; Score 597; DB 10; Length 111;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWATFOQKHINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61  
DB 3 NWATFOQKHINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 62  
QY 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRCP 110  
DB 63 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRCP 111

## RESULT 7

US-09-961-400-26

; Sequence 26, Application US/09961400  
; Publication No. US20030124131A1  
; GENERAL INFORMATION:  
; APPLICANT: RYBAK, SUSANNA M.  
; APPLICANT: GOLDENBERG, DAVID M.  
; APPLICANT: NEWTON, DIANNE L.  
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
; TITLE OF INVENTION: CELLS  
; FILE REFERENCE: 018733/1059  
; CURRENT APPLICATION NUMBER: US/09/961,400  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 60/079,751  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 111  
; TYPE: PRT  
; ORGANISM: Rana catesbeiana  
US-09-961-400-26

Query Match  
Best Local Similarity 99.2%; Score 597; DB 10; Length 111;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWATFOQKHINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61  
DB 3 NWATFOQKHINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 62  
QY 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRCP 110  
DB 63 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRCP 111

## RESULT 8

US-09-961-400-19  
; Sequence 19, Application US/09961400  
; Publication No. US20030124131A1  
; GENERAL INFORMATION:  
; APPLICANT: RYBAK, SUSANNA M.  
; APPLICANT: GOLDENBERG, DAVID M.  
; APPLICANT: NEWTON, DIANNE L.  
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
; TITLE OF INVENTION: CELLS  
; FILE REFERENCE: 018733/1059  
; CURRENT APPLICATION NUMBER: US/09/961,400  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 60/079,751  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Rana catesbeiana  
US-09-961-400-19

Query Match  
Best Local Similarity 99.0%; Score 596; DB 10; Length 110;  
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db 1 QNWATFOQKHINTPIICNTIMDNNTIYVGGQCKRVNTFISSATTVKAICTGVINNVNL 60  
QY 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 110  
Db 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 110

## RESULT 2

US-09-961-400-15  
; Sequence 15, Application US/09961400  
; Publication No. US20030124131A1  
; GENERAL INFORMATION:  
; APPLICANT: RYBAK, SUSANNA M.  
; APPLICANT: GOLDENBERG, DAVID M.  
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
; TITLE OF INVENTION: CELLS  
; FILE REFERENCE: 018733/1059  
; CURRENT APPLICATION NUMBER: US/09/961,400  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 60/079,751  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Rana catesbeiana  
US-09-961-400-15

Query Match 100.0%; Score 602; DB 10; Length 110;  
Best Local Similarity 100.0%; Pred. No. 9.5e-61;  
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 110

## RESULT 3

US-09-961-400-17  
; Sequence 17, Application US/09961400  
; Publication No. US20030124131A1  
; GENERAL INFORMATION:  
; APPLICANT: RYBAK, SUSANNA M.  
; APPLICANT: GOLDENBERG, DAVID M.  
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
; TITLE OF INVENTION: CELLS  
; FILE REFERENCE: 018733/1059  
; CURRENT APPLICATION NUMBER: US/09/961,400  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 60/079,751  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 111  
; TYPE: PRT  
; ORGANISM: Rana catesbeiana  
US-09-961-400-17

Query Match 100.0%; Score 602; DB 10; Length 111;  
Best Local Similarity 100.0%; Pred. No. 9.6e-61;  
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 62 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 111

## RESULT 4

US-09-948-391A-24  
; Sequence 24, Application US/09948391A  
; Publication No. US20030027311A1  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: The United States of America  
; APPLICANT: as represented by the Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Recombinant Anti-tumor RNase  
; FILE REFERENCE: 015280-343110US  
; CURRENT APPLICATION NUMBER: US/09/948,391A  
; CURRENT FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: US 60/079,751  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: US 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Rana  
; OTHER INFORMATION: catesbeiana ribonuclease with Gln1Ser substitution  
; OTHER INFORMATION: (recombinant RaCOR1 Q1S)  
US-09-948-391A-24

Query Match 99.2%; Score 597; DB 10; Length 110;  
Best Local Similarity 100.0%; Pred. No. 3.5e-60;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 110

## RESULT 5

US-09-961-400-24  
; Sequence 24, Application US/09961400  
; Publication No. US20030124131A1  
; GENERAL INFORMATION:  
; APPLICANT: RYBAK, SUSANNA M.  
; APPLICANT: GOLDENBERG, DAVID M.  
; APPLICANT: NEWTON, DIANNE L.  
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
; TITLE OF INVENTION: CELLS  
; FILE REFERENCE: 018733/1059  
; CURRENT APPLICATION NUMBER: US/09/961,400  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 09/622,613

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:40 ; Search time 35.2947 Seconds  
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Perfect score: 602  
Sequence: 1 QNWATFOQKHINTPIICNT.....ICVKENQYVHFAGIGRCP 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Description	
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2	602	100.0	110	US-09-961-400-15	Sequence 15, Appl
3	602	100.0	111	US-09-961-400-17	Sequence 17, Appl
4	597	99.2	110	US-09-948-391A-24	Sequence 24, Appl
5	597	99.2	110	US-09-961-400-24	Sequence 24, Appl
6	597	99.2	111	US-09-948-391A-26	Sequence 26, Appl
7	597	99.2	111	US-09-961-400-26	Sequence 26, Appl
8	596	99.0	110	US-09-961-400-19	Sequence 19, Appl
9	596	99.0	111	US-09-948-391A-17	Sequence 17, Appl
10	596	99.0	111	US-09-948-391A-21	Sequence 21, Appl
11	596	99.0	111	US-09-961-400-21	Sequence 21, Appl
12	596	99.0	117	US-09-948-391A-22	Sequence 22, Appl
13	596	99.0	117	US-09-961-400-22	Sequence 22, Appl
14	590	98.0	110	US-09-948-391A-19	Sequence 19, Appl
15	281.5	46.8	104	US-09-961-400-2	Sequence 2, Appl

16	281.5	46.8	105	10	US-09-948-391A-6	Sequence 6, Appl
17	281.5	46.8	105	10	US-09-961-400-6	Sequence 6, Appl
18	281.5	46.8	127	10	US-09-948-391A-28	Sequence 28, Appl
19	281.5	46.8	127	10	US-09-961-400-28	Sequence 28, Appl
20	280.5	46.6	104	10	US-09-948-391A-2	Sequence 2, Appl
21	278.5	46.3	111	10	US-09-961-400-9	Sequence 9, Appl
22	277.5	46.1	105	14	US-10-153-882-2	Sequence 11, Appl
23	276.5	45.9	104	10	US-09-948-391A-11	Sequence 11, Appl
24	276.5	45.9	104	10	US-09-961-400-11	Sequence 11, Appl
25	276.5	45.9	105	10	US-09-948-391A-13	Sequence 13, Appl
26	276.5	45.9	105	10	US-09-961-400-13	Sequence 13, Appl
27	275.5	45.8	104	10	US-09-948-391A-4	Sequence 4, Appl
28	275.5	45.8	104	10	US-09-961-400-4	Sequence 4, Appl
29	275.5	45.8	105	10	US-09-961-400-8	Sequence 8, Appl
30	272.5	45.3	104	9	US-09-986-119-1	Sequence 1, Appl
31	272.5	45.3	104	9	US-09-918-887-1	Sequence 1, Appl
32	269.5	44.8	104	12	US-10-461-713-53	Sequence 53, Appl
33	266.5	44.3	105	10	US-09-948-391A-8	Sequence 8, Appl
34	266.5	44.3	111	10	US-09-948-391A-9	Sequence 9, Appl
35	206	34.2	83	9	US-09-986-119-3	Sequence 3, Appl
36	206	34.2	83	10	US-09-918-887-3	Sequence 3, Appl
37	163	27.1	169	13	US-10-016-447-2	Sequence 2, Appl
38	135.5	22.5	124	12	US-10-037-417-103	Sequence 103, App
39	131.5	21.8	119	12	US-10-016-248-89	Sequence 89, Appl
40	131.5	21.8	119	15	US-10-074-978A-139	Sequence 139, App
41	121	20.1	99	15	US-10-074-978A-141	Sequence 141, App
42	117.5	19.5	124	12	US-10-461-713-52	Sequence 52, Appl
43	117	19.4	147	9	US-09-731-872-254	Sequence 254, App
44	117	19.4	147	10	US-09-876-937-254	Sequence 8, Appl
45	114.5	19.0	124	9	US-09-981-286A-8	

ALIGNMENTS

RESULT 1

US-09-948-391A-15  
; Sequence 15, Application US/09948391A  
; Publication No. US20030027311A1  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: The United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase  
; FILE REFERENCE: 015280-343110US  
; CURRENT APPLICATION NUMBER: US/09/948,391A  
; PRIOR FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: US 60/079,751  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: US 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Rana  
; OTHER INFORMATION: catesbiana oocyte ribonuclease (RaCOR1) synthetic  
; OTHER INFORMATION: gene modified to use E. coli preferred codons  
US-09-948-391A-15

Query Match 100.0%; Score 602; DB 10; Length 110;  
Best Local Similarity 100.0%; Pred. No. 9.5e-61;  
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNWATFOQKHINTPIICNTMDNNIYVGQCKRYNTFTISSATTVKATCTGVNNVVL 60  
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Sat May 8 17:57:17 2004

; ORGANISM: Rana pipiens  
US-09-961-400-9  
Query Match 46.6%; Score 279.5; DB 10; Length 111;  
Best Local Similarity 49.5%; Pred. No. 7.7e-24;  
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;  
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Db 64 VLTITSEFYLSDC---NVTISRECKYKLKSTNTFCVTCENQAPVHFVGVGHC 111

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Job time : 35.2947 secs

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; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1
; OTHER INFORMATION: and Gln2Ser substitution (Met(-1) RaCOR1 Q1S)
US-09-948-391A-26

Query Match      98.5%; Score 591; DB 10; Length 111;
Best Local Similarity 98.2%; Pred. No. 3.9e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY      62  TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
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RESULT 13
US-09-961-400-26
; Sequence 26, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-26

Query Match      98.5%; Score 591; DB 10; Length 111;
Best Local Similarity 98.2%; Pred. No. 3.9e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2  NWATFOQKHINTPIICNTLDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61
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QY      62  TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db      63  TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 14
US-09-948-391A-17
; Sequence 17, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1
; OTHER INFORMATION: (recombinant Met(-1) RaCOR1)
US-09-948-391A-17

Query Match      98.3%; Score 590; DB 10; Length 111;
Best Local Similarity 97.3%; Pred. No. 5e-59;
Matches 107; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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RESULT 15
US-09-961-400-9
; Sequence 9, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 111
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Db 62 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 9  
US-09-948-391A-19  
; Sequence 19, Application US/09948391A  
; Publication No. US20030027311A1  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: The United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase  
; FILE REFERENCE: 015280-343110US  
; CURRENT APPLICATION NUMBER: US/09/948,391A  
; PRIOR FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: US 60/079,751  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: US 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Rana  
; OTHER INFORMATION: catesbeiana ribonuclease with Met22Leu and  
; OTHER INFORMATION: Met57Leu substitutions (recombinant RacOR1  
; OTHER INFORMATION: Met22Leu Met57Leu)  
US-09-948-391A-19

Query Match 99.0%; Score 594; DB 10; Length 110;  
Best Local Similarity 99.1%; Pred. No. 1.7e-59;  
Matches 109; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 QNWATFQKHIIINTPIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINNVLS 60  
Db 1 QNWATFQKHIIINTPIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINNVLS 60

QY 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
Db 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
RESULT 10  
US-09-948-391A-24  
; Sequence 24, Application US/09948391A  
; Publication No. US20030027311A1  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: The United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase  
; FILE REFERENCE: 015280-343110US  
; CURRENT APPLICATION NUMBER: US/09/948,391A  
; PRIOR FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: US 60/079,751  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: US 09/622,613  
; PRIOR FILING DATE: 2000-08-17

; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Rana  
; OTHER INFORMATION: catesbeiana ribonuclease with Gln1Ser substitution  
; OTHER INFORMATION: (recombinant RacOR1 Q1S)  
US-09-948-391A-24

Query Match 98.5%; Score 591; DB 10; Length 110;  
Best Local Similarity 98.2%; Pred. No. 3.8e-59;  
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 2 NWATFQKHIIINTPIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINNVLS 61  
Db 2 NWATFQKHIIINTPIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINNVLS 61

QY 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
Db 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
RESULT 11  
US-09-961-400-24  
; Sequence 24, Application US/09961400  
; Publication No. US20030124131A1  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: GOLDENBERG, DAVID M.  
; APPLICANT: NEWTON, DIANNE L.  
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
; TITLE OF INVENTION: CELLS  
; FILE REFERENCE: 018733/1059  
; CURRENT APPLICATION NUMBER: US/09/961,400  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 60/079,751  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Rana catesbeiana  
US-09-961-400-24

Query Match 98.5%; Score 591; DB 10; Length 110;  
Best Local Similarity 98.2%; Pred. No. 3.8e-59;  
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 2 NWATFQKHIIINTPIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINNVLS 61  
Db 2 NWATFQKHIIINTPIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINNVLS 61

QY 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
Db 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
RESULT 12  
US-09-948-391A-26  
; Sequence 26, Application US/09948391A  
; Publication No. US20030027311A1  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: The United States of America

; CURRENT FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 60/079,751  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Rana catesbeiana  
US-09-961-400-22

Query Match 100.0%; Score 600; DB 10; Length 117;  
Best Local Similarity 100.0%; Pred. No. 3.9e-60;  
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNV 60  
Db 8 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNV 67  
Qy 61 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
Db 68 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117

RESULT 6  
US-09-948-391A-15  
; Sequence 15, Application US/09948391A  
; Publication No. US20030027311A1  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase  
; FILE REFERENCE: 015280-343110US  
; CURRENT APPLICATION NUMBER: US/09/948,391A  
; CURRENT FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: US 60/079,751  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: US 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Rana  
; OTHER INFORMATION: catesbeiana oocyte ribonuclease (RaCOR1) synthetic  
; OTHER INFORMATION: gene modified to use E. coli preferred codons  
US-09-948-391A-15

Query Match 99.3%; Score 596; DB 10; Length 110;  
Best Local Similarity 98.2%; Pred. No. 1e-59;  
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNV 60  
Db 1 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNV 60  
Qy 61 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
Db 61 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

Query Match 99.3%; Score 596; DB 10; Length 110;  
Best Local Similarity 98.2%; Pred. No. 1e-59;  
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNV 60  
Db 1 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNV 60  
Qy 61 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
Db 61 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 7  
US-09-961-400-15  
; Sequence 15, Application US/09961400  
; Publication No. US20030124131A1  
; GENERAL INFORMATION:  
; APPLICANT: RYBAK, SUSANNA M.  
; APPLICANT: GOLDENBERG, DAVID M.  
; APPLICANT: NEWTON, DIANNE L.  
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
; FILE REFERENCE: 018733/1059  
; CURRENT APPLICATION NUMBER: US/09/961,400  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 60/079,751  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Rana catesbeiana  
US-09-961-400-15

Query Match 99.3%; Score 596; DB 10; Length 110;  
Best Local Similarity 98.2%; Pred. No. 1e-59;  
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNV 60  
Db 1 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNV 60  
Qy 61 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
Db 61 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 8  
US-09-961-400-17  
; Sequence 17, Application US/09961400  
; Publication No. US20030124131A1  
; GENERAL INFORMATION:  
; APPLICANT: RYBAK, SUSANNA M.  
; APPLICANT: GOLDENBERG, DAVID M.  
; APPLICANT: NEWTON, DIANNE L.  
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
; FILE REFERENCE: 018733/1059  
; CURRENT APPLICATION NUMBER: US/09/961,400  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 60/079,751  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 111  
; TYPE: PRT  
; ORGANISM: Rana catesbeiana  
US-09-961-400-17

Query Match 99.3%; Score 596; DB 10; Length 111;  
Best Local Similarity 98.2%; Pred. No. 1e-59;  
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNV 60  
Db 1 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNV 60  
Qy 61 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
Db 61 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

Sat May 8 17:57:17 2004

US-09-961-400-21

Query Match 100.0%; Score 600; DB 10; Length 111;  
Best Local Similarity 100.0%; Pred. No. 3.7e-60;  
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNWATFQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVAICTGVINLNL 60  
Db 2 QNWATFQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVAICTGVINLNL 61

QY 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
Db 62 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 4

US-09-948-391A-22  
; Sequence 22, Application US/09948391A  
; Publication No. US20030027311A1  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: The United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase  
; FILE REFERENCE: 015280-343110US  
; CURRENT APPLICATION NUMBER: US/09/948,391A  
; CURRENT FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: US 60/079,751  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: US 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Rana  
; OTHER INFORMATION: catesbeiana ribonuclease with (His)6 tag, Met at  
; OTHER INFORMATION: position 7, Met23Leu and Met58Leu substitutions  
; OTHER INFORMATION: (recombinant Met(-1) RacOR1 Met22Leu Met57Leu-(His)6)  
US-09-948-391A-22

Query Match 100.0%; Score 600; DB 10; Length 117;  
Best Local Similarity 100.0%; Pred. No. 3.9e-60;  
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNWATFQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVAICTGVINLNL 60  
Db 8 QNWATFQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVAICTGVINLNL 67

QY 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
Db 68 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117

RESULT 5

US-09-961-400-22  
; Sequence 22, Application US/09961400  
; Publication No. US20030124131A1  
; GENERAL INFORMATION:  
; APPLICANT: RYBAK, SUSANNA M.  
; APPLICANT: GOLDENBERG, DAVID M.  
; APPLICANT: NEWTON, DIANNE L.  
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
; TITLE OF INVENTION: CELLS  
; FILE REFERENCE: 018733/1059  
; CURRENT APPLICATION NUMBER: US/09/961,400

RESULT 2

US-09-948-391A-21  
; Sequence 21, Application US/09948391A  
; Publication No. US20030027311A1  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: The United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase  
; FILE REFERENCE: 015280-343110US  
; CURRENT APPLICATION NUMBER: US/09/948,391A  
; CURRENT FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: US 60/079,751  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: US 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 111  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Rana  
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1,  
; OTHER INFORMATION: Met23Leu and Met58Leu substitutions (recombinant  
; OTHER INFORMATION: Met(-1) RacOR1 Met22Leu Met57Leu)  
US-09-948-391A-21

Query Match 100.0%; Score 600; DB 10; Length 111;  
Best Local Similarity 100.0%; Pred. No. 3.7e-60;  
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNWATFQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVAICTGVINLNL 60  
Db 2 QNWATFQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVAICTGVINLNL 61

QY 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
Db 62 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 3

US-09-961-400-21  
; Sequence 21, Application US/09961400  
; Publication No. US20030124131A1  
; GENERAL INFORMATION:  
; APPLICANT: RYBAK, SUSANNA M.  
; APPLICANT: GOLDENBERG, DAVID M.  
; APPLICANT: NEWTON, DIANNE L.  
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
; TITLE OF INVENTION: CELLS  
; FILE REFERENCE: 018733/1059  
; CURRENT APPLICATION NUMBER: US/09/961,400  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 60/079,751  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 111  
; TYPE: PRT  
; ORGANISM: Rana catesbeiana

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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:40 ; Search time 35.2947 Seconds  
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Title: US-09-961-400-19  
Perfect score: 600  
Sequence: 1 QNWATFOQKHINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1140673 seqs, 277566755 residues  
Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
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8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
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16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	600	100.0	110	10	US-09-961-400-19
2	600	100.0	111	10	US-09-948-391A-21
3	600	100.0	111	10	US-09-961-400-21
4	600	100.0	117	10	US-09-948-391A-22
5	600	100.0	117	10	US-09-961-400-22
6	596	99.3	110	10	US-09-948-391A-15
7	596	99.3	110	10	US-09-961-400-15
8	596	99.3	111	10	US-09-961-400-17
9	594	99.0	110	10	US-09-948-391A-19
10	591	98.5	110	10	US-09-948-391A-24
11	591	98.5	110	10	US-09-961-400-24
12	591	98.5	111	10	US-09-948-391A-26
13	591	98.5	111	10	US-09-961-400-26
14	590	98.3	111	10	US-09-948-391A-17
15	279.5	46.6	111	10	US-09-961-400-9

## SUMMARIES

16	277.5	46.2	104	10	US-09-961-400-2	Sequence 2, Appli
17	277.5	46.2	105	10	US-09-948-391A-6	Sequence 6, Appli
18	277.5	46.2	105	10	US-09-961-400-6	Sequence 6, Appli
19	277.5	46.2	127	10	US-09-948-391A-28	Sequence 28, Appli
20	277.5	46.2	127	10	US-09-961-400-28	Sequence 2, Appli
21	276.5	46.1	104	10	US-09-948-391A-2	Sequence 4, Appli
22	276.5	46.1	104	10	US-09-948-391A-4	Sequence 8, Appli
23	276.5	46.1	104	10	US-09-961-400-8	Sequence 2, Appli
24	276.5	46.1	105	10	US-09-961-400-4	Sequence 4, Appli
25	273.5	45.6	105	14	US-10-153-882-2	Sequence 8, Appli
26	272.5	45.4	104	10	US-09-948-391A-11	Sequence 2, Appli
27	272.5	45.4	104	10	US-09-961-400-11	Sequence 11, Appl
28	272.5	45.4	104	10	US-09-948-391A-13	Sequence 11, Appl
29	272.5	45.4	105	10	US-09-961-400-13	Sequence 13, Appl
30	268.5	44.8	104	9	US-09-986-119-1	Sequence 1, Appli
31	268.5	44.8	104	10	US-09-918-887-1	Sequence 1, Appli
32	267.5	44.6	105	10	US-09-948-391A-8	Sequence 8, Appli
33	267.5	44.6	111	10	US-09-948-391A-9	Sequence 9, Appli
34	265.5	44.2	104	12	US-10-461-713-53	Sequence 53, Appl
35	202	33.7	83	9	US-09-986-119-3	Sequence 3, Appli
36	202	33.7	83	10	US-09-918-887-3	Sequence 3, Appli
37	161	26.8	169	13	US-10-016-447-2	Sequence 2, Appli
38	131.5	21.9	124	12	US-10-037-417-103	Sequence 103, App
39	127.5	21.2	119	12	US-10-016-248-89	Sequence 89, Appl
40	127.5	21.2	119	15	US-10-074-378A-139	Sequence 139, App
41	118	19.7	99	15	US-10-074-378A-141	Sequence 141, App
42	117	19.5	147	9	US-09-731-872-254	Sequence 254, App
43	117	19.5	147	10	US-09-876-997-254	Sequence 254, App
44	114	19.0	123	12	US-10-461-713-58	Sequence 58, Appl
45	114	19.0	124	13	US-10-016-447-5	Sequence 5, Appli

## ALIGNMENTS

## RESULT 1

US-09-961-400-19  
; Sequence 19, Application US/09961400  
; Publication No. US20030124131A1  
; GENERAL INFORMATION:  
; APPLICANT: RYBAK, SUSANNA M.  
; APPLICANT: GOLDENBERG, DAVID M.  
; APPLICANT: NEWTON, DIANNE L.  
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
; TITLE OF INVENTION: CELLS  
; FILE REFERENCE: 018733/1059  
; CURRENT APPLICATION NUMBER: US/09/961,400  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 60/079,751  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Rana catesbeiana  
US-09-961-400-19

Query Match	100.0%	Score	600	DB	10	Length	110
Best Local Similarity	100.0%	Pred. No.	3.7e-60				
Matches	110	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
QY	1	QNWATFOQKHINTPIICNTILDNNIYVGGCKVNTFISSATTVAICTGVINLVL	60				
Db	1	QNWATFOQKHINTPIICNTILDNNIYVGGCKVNTFISSATTVAICTGVINLVL	60				
QY	61	STTRFQNLCTRTSTTPPCYSSRTETNYICVKCENQYPVHFAGIGRCP	110				
Db	61	STTRFQNLCTRTSTTPPCYSSRTETNYICVKCENQYPVHFAGIGRCP	110				



Sat May 8 17:57:15 2004

RA Hooper L.V., Stappenbeck T.S., Hong C.V., Gordon J.I.;  
 RT "Angiogenins: a new class of microbicidal proteins involved in innate  
 immunity.";  
 RL Nat. Immunol. 4:269-273(2003).  
 DR EMBL; AY219670; AAC62354.1; -  
 DR GO; GO:0003676; F:nucleic acid binding; IEA.  
 DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.  
 DR InterPro; IPR001427; RNaseA.  
 DR Pfam; PF00074; rnaseA; 1.  
 DR PRINTS; PR00794; RIBONUCLEASE.  
 DR ProDom; PD000535; RNaseA; 1.  
 DR SMART; SM00092; RNase\_Pc; 1.  
 DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
 SQ SEQUENCE 144 AA; 16554 MW; 09808807C00224C1 CRC64;

Query Match 21.3%; Score 128.5; DB 11; Length 144;  
 Best Local Similarity 38.2%; Pred. No. 4.6e-07;  
 Matches 29; Conservative 13; Mismatches 29; Indels 5; Gaps 3;  
 QY 33 CKRVNTEFIISATTVKAIC--TGVINMNV-LSTTRPOLNCTRTSTTP-RPCYSSRTE 87  
 Db 62 CKDNTFIHGTCKNIRAICGKSGPYGENFRISNPFQITTCTHSRGSPWPCGYRAFKD 121  
 QY 88 TNVICVKENQYVPHF 103  
 Db 122 FRVIYIACEDGWPVHF 137

Search completed: May 7, 2004, 21:46:03  
 Job time : 31.2816 secs

Q9BEC1 PRELIMINARY; PRT; 170 AA.  
 AC Q9BEC1;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Brain-type ribonuclease ribonuclease precursor (Fragment).  
 GN RNase B.  
 OS Tragus javanicus (Lesser Malay chevronetain).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Tragulina;  
 OC Tragulidae; Tragulus.  
 OX NCBI\_TaxID=9849;  
 RN [1]  
 RZ SEQUENCE FROM N.A.  
 RX MEDLINE=21347458; PubMed=11453981;  
 RA Breukelman H.J., Jekel P.A., Dubois J.Y., Mulder P.P.M.F.A.,  
 RA Warmels H.W., Beintema J.J.;  
 RT "Secretory ribonucleases in the primitive ruminant chevrotain  
 (Tragus javanicus).";  
 RL Eur. J. Biochem. 268:3890-3897(2001).  
 CC -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 DR EMBL; AJ271299; CAB24723.1; -  
 DR HSP; P00656; ILQO.  
 DR GO; GO:0004519; F:endonuclease activity; IEA.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.  
 DR InterPro; IPR001427; RNaseA.  
 DR Pfam; PF00074; rnaseA; 1.  
 DR PRINTS; PR00794; RIBONUCLEASE.  
 DR ProDom; PD000535; RNaseA; 1.  
 DR SMART; SM00092; RNase\_Pc; 1.  
 DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
 KW Endonuclease; Hydrolase; Nuclease; Signal.  
 FT SIGNAL  
 FT NON TER 1 1  
 FT CHAIN 20 170 BRAIN-TYPE RIBONUCLEASE RIBONUCLEASE.  
 SQ SEQUENCE 170 AA; 18832 MW; ABCE7E1B5549AA0 CRC64;

Query Match 21.8%; Score 131; DB 6; Length 170;  
 Best Local Similarity 33.1%; Pred. No. 2.8e-07;  
 Matches 41; Conservative 17; Mismatches 46; Indels 20; Gaps 7;

QY 4 ATFOQKH-----INTPIICNTINDNNIYVGGCKRVNTEFIISATTVKAICT----- 52  
 Db 25 AKFRQHLHDAGNSINSN-YCNLMKKRR-KMTHGRCKPVNFIHESLEDVKAICSEKNIT 82  
 QY 53 ---GVINMNVLTTRPOLNCTRTSTTP-RPCYSSRTEYICVKEN--QYPVHFAGI 106  
 Db 83 CKNGQPNCHQSNT-MNITDCRQTGSGKYPCAYKTSQKQYIIVACEGTPSPVPHFDGS 141  
 QY 107 GRCP 110  
 Db 142 AVLP 145

RESULT 15  
 Q80Z85 PRELIMINARY; PRT; 144 AA.  
 ID Q80Z85  
 AC Q80Z85;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Angiogenin-4.  
 GN ANG4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RZ SEQUENCE FROM N.A.  
 RX STRAIN=NMRI;  
 MEDLINE=22493143; PubMed=12548285;

RESULT 11	
Q9DFY7	
ID	Q9DFY7 PRELIMINARY; PRT; 128 AA.
AC	Q9DFY7;
DT	01-MAR-2001 (TrEMBLrel. 16, Created)
DT	01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	RC-RNase3 ribonuclease precursor.
OS	Rana catesbeiana (Bull frog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX	NCBI_TaxID=8400;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Liver;
RX	MEDLINE=20512555; PubMed=11058105;
RA	Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT	"Purification and cloning of cytotoxic ribonucleases from Rana
RT	catesbeiana (bullfrog).";
RL	Nucleic Acids Res. 28:4097-4104(2000).
DR	EMBL; AF242554; AAG31440.2; -.
DR	HSSP; P22069; 10NC.
DR	GO; GO:0003676; P:nucleic acid binding; IEA.
DR	GO; GO:0004522; P:pancreatic ribonuclease activity; IEA.
DR	InterPro; IPR001427; RNaseA.
DR	Pfam; PF00074; rNaseA; 1.
DR	ProDom; PD000535; rNaseA; 1.
DR	PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW	Signal.
FT	SIGNAL. 1 23 POTENTIAL.
FT	CHAIN 24 128 RC-RNASE3 RIBONUCLEASE.
SQ	SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;
Query Match 37.6%; Score 226.5; DB 13; Length 128;	
Best Local Similarity 41.1%; Pred. No. 1.5e-18;	
Matches 46; Conservative 18; Mismatches 39; Indels 9; Gaps 4;	
Qy	1 QNWATFQOKHLINT-PIICNTIMDNIIYVGQCKRYNTFTISSATVTKALCTGV-INMN 58
Db	24 QDWETFQCKHLTDTKYKCVEMAKALF----DCKNTFTIYALPGRYKALCKNRDNTD 79
Qy	59 VLSRTFRQLNCTRTSITPRPCPYSSRTETNYICVKENQYVHPAGIGRCP 110
Db	80 VLSRDAFLLPQCDRIKL--PCHYKLSSNTICITCNQLPIHFAGVGSCTP 128
RESULT 12	
Q9DFY5	
ID	Q9DFY5 PRELIMINARY; PRT; 128 AA.
AC	Q9DFY5;
DT	01-MAR-2001 (TrEMBLrel. 16, Created)
DT	01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	RC-RNase6 ribonuclease precursor.
OS	Rana catesbeiana (Bull frog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX	NCBI_TaxID=8400;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Liver;
RX	MEDLINE=20512555; PubMed=11058105;
RA	Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT	"Purification and cloning of cytotoxic ribonucleases from Rana
RT	catesbeiana (bullfrog).";
RL	Nucleic Acids Res. 28:4097-4104(2000).
DR	EMBL; AF242556; AAG31442.2; -.
DR	HSSP; P22069; 10NC.
DR	GO; GO:0003676; P:nucleic acid binding; IEA.
DR	GO; GO:0004522; P:pancreatic ribonuclease activity; IEA.
DR	InterPro; IPR001427; RNaseA.
DR	Pfam; PF00074; rNaseA; 1.
DR	ProDom; PD000535; rNaseA; 1.
DR	PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW	Signal.
FT	SIGNAL. 1 23 POTENTIAL.
FT	CHAIN 24 128 RC-RNASE3 RIBONUCLEASE.
SQ	SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;
Query Match 37.6%; Score 226.5; DB 13; Length 128;	
Best Local Similarity 41.1%; Pred. No. 1.5e-18;	
Matches 46; Conservative 18; Mismatches 39; Indels 9; Gaps 4;	
Qy	1 QNWATFQOKHLINT-PIICNTIMDNIIYVGQCKRYNTFTISSATVTKALCTGV-INMN 58
Db	24 QDWETFQCKHLTDTKYKCVEMAKALF----DCKNTFTIYALPGRYKALCKNRDNTD 79
Qy	59 VLSRTFRQLNCTRTSITPRPCPYSSRTETNYICVKENQYVHPAGIGRCP 110
Db	80 VLSRDAFLLPQCDRIKL--PCHYKLSSNTICITCNQLPIHFAGVGSCTP 128

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RESULT 8
Q8UVX5 PRELIMINARY; PRT; 127 AA.
ID Q8UVX5 AC Q8UVX5
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Onconase precursor.
GN RPR.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RN [2]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Wang S.-C.;
RT "Rana pipiens onconase genomic DNA.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332139; AAL54383.1; -.
DR PIR; A39035; A39035.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNasePc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL
FT SIGNAL
SQ SEQUENCE 127 AA; 14469 MW; 953F90D351CFEEF3 CRC64;

Query Match 46.1%; Score 277.5; DB 13; Length 127;
Best Local Similarity 49.5%; Pred. No. 1.7e-24;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NMN 58
Db 24 QWLTFQKHINTRDVDCNIMSNLFP-----HCKDKNTFIYSRPEPVKAICKGIASKN 79

QY 59 VLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 109
Db 80 VLTTFEYILSDC---NVTSRCKYKLLKSKTNKFCVTCENQAPVHFVGVGSC 127

RESULT 9
Q9DFY6 PRELIMINARY; PRT; 129 AA.
ID Q9DFY6 AC Q9DFY6
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE RC-RNase4 ribonuclease precursor.
OS Rana catesbeiana (bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RN [2]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104 (2000).
RN [1]
RN [2]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242553; AAG31439.1; -.
DR PDB; 1M58; 09-JAN-03.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL
FT SIGNAL
SQ SEQUENCE 128 AA; 14839 MW; 989719CF52053ECC CRC64;

Query Match 38.1%; Score 229.5; DB 13; Length 128;
Best Local Similarity 40.2%; Pred. No. 6.7e-19;
Matches 45; Conservative 20; Mismatches 38; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NMN 58
Db 24 QWWEIFQKHILTRDVKDAEMKALF---DCKDKNTFIYARPGRVQALCKNIIVSKN 79

QY 59 VLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 80 VLSTDFYILSDCNRIKL---PCHYKLLKSSNTICITCENKLPVHFVAVEECP 128

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InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL
FT CHAIN
FT CHAIN
SQ SEQUENCE 129 AA; 14724 MW; 826A62882B10ABDA CRC64;

Query Match 40.9%; Score 246; DB 13; Length 129;
Best Local Similarity 43.4%; Pred. No. 8e-21;
Matches 49; Conservative 24; Mismatches 30; Indels 10; Gaps 5;

QY 1 QNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NMN 58
Db 24 QDWATFKKHLTDTWDVDCNLMPTSLF---DCKDKNTFIYSLPGFVKALCRGVIFSD 79

QY 59 VLSTTRFQNLCTRTSITPR-PCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 80 VLSNSEFYLAEC---NVKPRKPKYKLLKSSNRICIRCEHELPHVHFAGVGLCP 129

RESULT 10
Q9DFY8 PRELIMINARY; PRT; 128 AA.
ID Q9DFY8 AC Q9DFY8
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE RC-RNase2 ribonuclease precursor.
OS Rana catesbeiana (bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104 (2000).
RN [1]
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242553; AAG31439.1; -.
DR PDB; 1M58; 09-JAN-03.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL
FT CHAIN
FT CHAIN
SQ SEQUENCE 128 AA; 14839 MW; 989719CF52053ECC CRC64;

Query Match 38.1%; Score 229.5; DB 13; Length 128;
Best Local Similarity 40.2%; Pred. No. 6.7e-19;
Matches 45; Conservative 20; Mismatches 38; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NMN 58
Db 24 QWWEIFQKHILTRDVKDAEMKALF---DCKDKNTFIYARPGRVQALCKNIIVSKN 79

QY 59 VLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 80 VLSTDFYILSDCNRIKL---PCHYKLLKSSNTICITCENKLPVHFVAVEECP 128

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RESULT 5
Q98SM1 ID Q98SM1 PRELIMINARY; PRT; 132 AA.
AC DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc204 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351208; AAK30254.1; -.
DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;

Query Match
Best Local Similarity 74.5%; Score 448.5; DB 13; Length 132;
Matches 86; Conservative 7; Mismatches 16; Indels 1; Gaps 1;

QY 1 QNWATFOQKHINTPII-CNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 59
Db 23 QDWPTFOQKHIPSTSSIDCNTIMDKIYVIRGQCKVNTFIYSATTVKAICTGVINNV 82

QY 60 LSTTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYVPHFAGIGRC 109
Db 83 LSTTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYVPHFAGIGRC 127

RESULT 6
Q9DF78 ID Q9DF78 PRELIMINARY; PRT; 132 AA.
AC DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RC-RNaseL1 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RA Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288642; AAG30414.2; -.

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DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 132 AA; 14625 MW; D8D9A517452PBE53 CRC64;

Query Match
Best Local Similarity 62.5%; Score 376; DB 13; Length 132;
Matches 73; Conservative 9; Mismatches 27; Indels 2; Gaps 2;

QY 1 QNWATFOQKHINTPII-CNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NMN 58
Db 22 QWAKFKKHITSTSSIDCNTIMDKAIYVGGCKKERTFTIISSEDNVKAICGVSPPDK 81

QY 59 VLSTTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYVPHFAGIGRC 109
Db 82 ELSTTSFKLNTCIRDSTPRCPYHPSPDNNKICVCKEQLPVHFGVIGKC 132

RESULT 7
Q918V8 ID Q918V8 PRELIMINARY; PRT; 127 AA.
AC DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Onconase variant rap1R1 precursor.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA MEDLINE=20330357; PubMed=10871370;
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
RT 3' UTR of unusual length and structure.";
RL Nucleic Acids Res. 28:2375-2382(2000).
DR EMBL; AF165133; AAF76935.1; -.
DR PIR; A39035; A39035.
DR HSSP; P22069; 1ONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;

Query Match
Best Local Similarity 46.8%; Score 281.5; DB 13; Length 127;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINTPII-CNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NMN 58
Db 24 QDWLTFQKHINTTRDVCNNIMSNLF----HCKDKNTFIYSRPFVKAICGIIASKN 79

QY 59 VLSTTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYVPHFAGIGRC 109
Db 80 VLTTSEFYLSDC---NVTSRPKYKLKSTNTFCVTCENQAPVHFGVGHG 127

```



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:10 ; Search time 31.2816 Seconds  
(without alignments)  
1109.503 Million cell updates/sec

Title: US-09-961-400-15

Perfect score: 602

Sequence: 1 QNWATFQCKHINTPII...ICVKCENQYVHFAGTGRCP 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL 25:\*
- 1: sp\_archaea:\*
  - 2: sp\_bacteria:\*
  - 3: sp\_fungi:\*
  - 4: sp\_human:\*
  - 5: sp\_invertebrate:\*
  - 6: sp\_mammal:\*
  - 7: sp\_mhc:\*
  - 8: sp\_organelle:\*
  - 9: sp\_phase:\*
  - 10: sp\_plant:\*
  - 11: sp\_rodent:\*
  - 12: sp\_virus:\*
  - 13: sp\_vertebrate:\*
  - 14: sp\_unclassified:\*
  - 15: sp\_rvirus:\*
  - 16: sp\_bacteriap:\*
  - 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	560.5	93.1	133	13	Q98SM0 rana catesb
2	487.5	81.0	132	13	Q98SM2 rana catesb
3	478.5	79.5	133	13	Q98SL9 rana catesb
4	471.5	78.3	133	13	Q98SL8 rana catesb
5	448.5	74.5	132	13	Q98SM1 rana catesb
6	376	62.5	132	13	Q9DF78 rana catesb
7	281.5	46.8	127	13	Q918V8 rana catesb
8	277.5	46.1	127	13	Q8UVX5 rana pipien
9	246	40.9	129	13	Q9DFY6 rana catesb
10	229.5	38.1	128	13	Q9DFY8 rana catesb
11	226.5	37.6	128	13	Q9DFY7 rana catesb
12	217.5	36.1	128	13	Q9DFY5 rana catesb
13	163	27.1	169	13	Q9W738 xenopus lae
14	131	21.8	170	6	Q9BEC1
15	128.5	21.3	144	11	Q80Z85
16	128.5	21.3	153	11	Q80XS4

17	127.5	21.2	147	6	Q7YR76	Q7YR76 balaena mys
18	126	20.9	150	11	Q8VD94	Q8VD94 berylmys bo
19	125.5	20.8	163	6	Q9BDC2	Q9BDC2 antilocapra
20	124.5	20.7	116	6	Q9TVC0	Q9TVC0 sus scrofa
21	124	20.6	150	11	Q8VD88	Q8VD88 rattus norv
22	122.5	20.3	144	6	Q9BH14	Q9BH14 antilocapra
23	121.5	20.2	147	6	Q7YR75	Q7YR75 tursiops tr
24	121	20.1	146	6	Q861Y5	Q861Y5 colobus gue
25	120.5	20.0	149	11	Q8K2T2	Q8K2T2 mus musculu
26	120.5	20.0	149	11	Q8C6G3	Q8C6G3 mus musculu
27	120	19.9	150	11	Q8VD92	Q8VD92 rattus exul
28	119.5	19.9	146	6	Q861Y4	Q861Y4 trachypithe
29	118.5	19.7	146	6	Q861Y3	Q861Y3 pygathrix r
30	118.5	19.7	146	6	Q861Y2	Q861Y2 pygathrix b
31	118.5	19.7	146	6	Q861Y1	Q861Y1 pygathrix a
32	116.5	19.4	152	11	Q8VD89	Q8VD89 rattus norv
33	114.5	19.0	124	6	Q9SNE6	Q9SNE6 bubalus bub
34	112.5	18.7	148	11	Q8C7E4	Q8C7E4 mus musculu
35	112.5	18.7	149	11	Q8VD95	Q8VD95 berylmys bo
36	112	18.6	134	6	Q9BDB9	Q9BDB9 tragulus ja
37	111.5	18.5	152	11	Q8VD84	Q8VD84 rattus tior
38	111.5	18.5	156	6	Q8SQ05	Q8SQ05 lagothrix l
39	111	18.4	148	11	Q8C6E3	Q8C6E3 mus musculu
40	110.5	18.4	119	6	Q9TV28	Q9TV28 eulemur ful
41	110.5	18.4	119	6	Q9TV30	Q9TV30 saguinus oe
42	109.5	18.2	142	6	Q9BEC3	Q9BEC3 tragulus ja
43	109.5	18.2	156	6	Q8SQ06	Q8SQ06 ateles geof
44	109	18.1	124	6	Q9BEC2	Q9BEC2 tragulus ja
45	108.5	18.0	156	6	Q8SQ08	Q8SQ08 saimiri sci

## ALIGNMENTS

## RESULT 1

Q98SM0	PRELIMINARY;	PRT;	133 AA.
ID	Q98SM0		
AC	Q98SM0;		
DT	01-JUN-2001 (TrEMBLrel. 17, Created)		
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)		
DE	RNase A-type ribonuclease rc208 precursor.		
DE	RNase A-type ribonuclease rc208 precursor.		
OS	Rana catesbeiana (Bull frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.		
OX	NCBI_TaxID=9400;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21539506; PubMed=11683320;		
RA	Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;		
RT	"Rapid diversification of RNase A superfamily ribonuclease from the		
RT	bullfrog, Rana catesbeiana."		
RL	J. Mol. Evol. 53:31-38(2001).		
DR	EMBL; AF351209; AAK30255.1; -		
DR	HSSP; P11915; 1BC4.		
DR	GO; GO:0003676; F:nucleic acid binding; IEA.		
DR	GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.		
DR	InterPro; IPR001427; RNaseA.		
DR	Pfam; PF00074; rnasea; 1.		
DR	ProDom; PD000535; RNaseA; 1.		
DR	SMART; SM00092; RNase_PC; 1.		
DR	PROSITE; PS00127; RNASE_PANCREATIC; 1.		
KW	SIGNAL.		
FT	SIGNAL		
SQ	SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;		

Query Match 93.1%; Score 560.5; DB 13; Length 133;  
Best Local Similarity 94.6%; Pred. No. 1.7e-57;  
Matches 105; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 QNWATFQCKHINTPII-CNTIMDNNIYVGQCKRVNTFISSATTVAICTGVIMNV 59  
DB 23 QNWATFQCKHINTPII-CNTIMDNNIYVGQCKRVNTFISSATTVAICTGVIMNV 82



CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
APPLICATION DATA:  
US 60/011,800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Paris, Susan K.  
REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 358 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-875-811-51

Query Match 45.8%; Score 277.5; DB 3; Length 358;  
Best Local Similarity 49.1%; Pred. No. 4.2e-24;  
Matches 55; Conservative 15; Mismatches 33; Indels 9; Gaps 4;

Qy 1 MSNWATFOOKHIINT-PIICNTIMDNNTIYVGGQCKRVNTFISSATTVKACTGVI-NM 58  
Db 1 MEDWLTFOKKHITNRDVCNIMTNLF----HCKDKNTFYSPPEPVKALCKGIIASK 56  
Qy 59 NVLTSTRFQLNCTRTSITPRCPYSSRTETNYICVKCENQYVHFAGIGRC 110  
Db 57 NVLTSTRFQLNCTRTSITPRCPYSSRTETNYICVKCENQYVHFAGIGRC 105

RESULT 14  
US-08-875-811-26  
Sequence 26, Application US/08875811  
Patent No. 6045793  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Boque, Lluís  
APPLICANT: Wlodawer, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
APPLICATION DATA:  
US 60/011,800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Paris, Susan K.  
REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-875-811-26

Query Match 45.6%; Score 276.5; DB 3; Length 105;  
Best Local Similarity 49.1%; Pred. No. 1.2e-24;  
Matches 55; Conservative 15; Mismatches 33; Indels 9; Gaps 4;

Qy 1 MSNWATFOOKHIINT-PIICNTIMDNNTIYVGGQCKRVNTFISSATTVKACTGVI-NM 58  
Db 1 MEDWLTFOKKHITNRDVCNIMTNLF----HCKDKNTFYSPPEPVKALCKGIIASK 56  
Qy 59 NVLTSTRFQLNCTRTSITPRCPYSSRTETNYICVKCENQYVHFAGIGRC 110  
Db 57 NVLTSTRFQLNCTRTSITPRCPYSSRTETNYICVKCENQYVHFAGIGRC 105

RESULT 15  
US-08-283-971-1  
Sequence 1, Application US/08283971  
Patent No. 5529775  
GENERAL INFORMATION:  
APPLICANT: Ardelt Ph.D, Wojciech J.  
APPLICANT: Mikulski, Stanislaw M.  
TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mark H. Jay, P.C.  
STREET: P.O. Box 020083, General Post Office  
CITY: Brooklyn  
STATE: New York  
COUNTRY: USA  
ZIP: 11202-0002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/283,971  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/921,180  
FILING DATE: 30-JUL-1992  
APPLICATION NUMBER: US 07/178,118  
FILING DATE: 06-APR-1988  
APPLICATION DATA:  
APPLICATION NUMBER: US 07/436,141  
FILING DATE: 13-NOV-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Jay, Mark H.  
REGISTRATION NUMBER: 27507  
REFERENCE/DOCKET NUMBER: 5006 US  
TELECOMMUNICATION INFORMATION:



Qy	1	MSNWATTCOKHHINT-PIICNTIMDNNIYIVGGQCKRVNTFISGATTVKATCTGVI-NM	58
Db	262	MSDWLTTCOKHHINTRDVDCDNIMSTNLF----HCKDKNFTIYSRPEPKATCKGIIASK	317
Qy	59	NVLSTTFPQLMCTCTSTIIPPCPSYSSSTETNIYIVCKENQYVHFAGIGRC	110
Db	318	NVLSTTSFYLGDC---NVTSPCKYKLLAKSTKNFCVTGENQAPVHFVGVGSC	366

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RESULT 11
US-08-875-811-39
; Sequence 39, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Iulius
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
;

```

ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA

```

, ZIP: 94111-3834
,
, COMPUTER READABLE FORM:
,
, MEDIUM TYPE: Floppy disk
,
, COMPUTER: IBM PC compatible
,
, OPERATING SYSTEM: PC-DOS/MS-DOS
,
, SOFTWARE: PatentIn Release #1.0, Version #1.30
,
, CURRENT APPLICATION DATA:
,
, APPLICATION NUMBER: US/08/875,811
,

```

FILING DATE: 19-FEB-1998  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA: WO PCT/US97/02588  
 APPLICATION NUMBER: 19-FEB-1997  
 FILING DATE: 19-FEB-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/011,800  
 FILING DATE: 21-FEB-1996  
 ATTORNEY/AGENT INFORMATION:

NAME: Paris, Susan K.  
REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300

```

; INFORMATION FOR SEQ ID NO: 39:
;
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 105 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
; US-08-875-811-39

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Query Match	45.8%	Score	277.5	DB 3	Length	105			
Best Local Similarity	49.1%	Pred. No.	9.4e-25						
Matches	55	Conservative	15	Mismatches	33	Indels	9	Gaps	4

Qy	1 MSNWATFQQKHIINT-PIICNTIMDNNIYVGGCKRVNTHFISSATTAKAICTGVI-NM 58   :             :   :   :           :     :             :   :   :           :
Db	1 MEDWLTFFQKKHITNTDFDVDCNIMSTNLF-----HCKDKNTFYISRPPEPVKAICKGIISK 56   :             :   :   :           :     :             :   :   :           :

**Q7** 59 NVLSTTRFQLNCTRTSITPRPCYGSRTETNYICVKCNQYPVHFAGIGRC 110  
|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
**D6** 57 NVLTISFYLSDC---NVSRPCKYIKKSTNKFCVTGNOAPVHFRVGVCSC 105

Db

RESULT 12  
US-08-875-811-41

```

: Sequence 41, Application US/08875811
: Patent No. 6045793
: GENERAL INFORMATION:
: APPLICANT: Rybak, Susanna M.
: APPLICANT: Newton, Dianne L.
: APPLICANT: Boque, Lluis
: APPLICANT: Wlodawer, Alexander
: TITLE OF INVENTION: Recombinant Ribonuclease Proteins
: NUMBER OF SEQUENCES: 64
: CORRESPONDENCE ADDRESS:
:

```

ADDRESS: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA

```

1  COMPANY: 035
2  ZIP: 94111-3834
3  COMPUTER READABLE FORM:
4  MEDIUM TYPE: Floppy disk
5  COMPUTER: IBM PC compatible
6  OPERATING SYSTEM: PC-DOS/MS-DOS
7  SOFTWARE: PatentIn Release #1.0, Version #1.30
8  CURRENT APPLICATION DATA:

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; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/875,811  
 ; FILING DATE: 19-FEB-1998  
 ; CLASSIFICATION: 435

PRIOR APPLICATION DATA: WO PCT/US97/02588

; FILING DATE: 19-FEB-1997  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/011,800

;  
; FILING DATE: 21-FEB-1996  
;  
; ATTORNEY/AGENT INFORMATION:  
;  
; NAME: Faris, Susan K.

; REGISTRATION NUMBER: 41,739  
 ; REFERENCE/DOCKET NUMBER: 015280-244100US  
 ; TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 41:

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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
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;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-08-875-811-41

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Query Match 45.8%; Score 277.5; DB 3; Length 355;  
Best Local Similarity 49.1%; Pred. No. 4.1e-24;  
Matches 55; Conservative 15; Mismatches 33; Indels 9

[illegible]

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RESULT 13
US-08-875-811-51
; Sequence 51, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluis
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor

```

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; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-57

Query Match          46.5%; Score 281.5; DB 3; Length 355;
Best Local Similarity 50.0%; Pred. No. 1.4e-24;
Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 MSNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NM 58
DB 1 MSDWLTFOKKHITNTDRDVCNDIMSTNLF---HCKDKNTFIYSRPEPVKAICKGLIASK 56

QY 59 NVLSTTRFQLNCTRTSITPRPCPYSSRTETNYICVKCENQVPHFAGIGRC 110
DB 57 NVLTTFSEFVLSDC--NVTSRCKYKLLKSTNKFVTCENQAPVHFVGVGSC 105

RESULT 9
US-08-875-811-64
; Sequence 64, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; APPLICATION DATA: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
```

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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..355
; OTHER INFORMATION: /note= "E6FB[Met-(-1)]SerrOnc"
; US-08-875-811-64

Query Match          46.5%; Score 281.5; DB 3; Length 355;
Best Local Similarity 50.0%; Pred. No. 1.4e-24;
Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 MSNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NM 58
DB 251 MSDWLTFOKKHITNTDRDVCNDIMSTNLF---HCKDKNTFIYSRPEPVKAICKGLIASK 306

QY 59 NVLSTTRFQLNCTRTSITPRPCPYSSRTETNYICVKCENQVPHFAGIGRC 110
DB 307 NVLTTFSEFVLSDC--NVTSRCKYKLLKSTNKFVTCENQAPVHFVGVGSC 355

RESULT 10
US-08-875-811-55
; Sequence 55, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; APPLICATION DATA: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 366 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-55

Query Match          46.5%; Score 281.5; DB 3; Length 366;
Best Local Similarity 50.0%; Pred. No. 1.5e-24;
Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
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```

; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-61

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Query Match 46.5%; Score 281.5; DB 3; Length 254;
Best Local Similarity 50.0%; Pred. No. 9.5e-25;
Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 MSNWATFQOKHIINT-PIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVI-NM 58
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MSDWLTFFQKHINTRDVDCDNIMSTNLF---HCKDKNTFIYSRPFVKAICKGIASK 56

QY 59 NVLSTTRFQNLCTRTSITPRPCPSYSRRTETNYICVKCENQYVHFAGIGRC 110
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 57 NVLTTFEFLSDC---NVTSRPCKYKLRKSTNKFVCVCENQAPVHFVGVGSC 105

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```

RESULT 7
US-08-875-811-49
; Sequence 49, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-49

Query Match 46.5%; Score 281.5; DB 3; Length 355;
Best Local Similarity 50.0%; Pred. No. 1.4e-24;
Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 MSNWATFQOKHIINT-PIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVI-NM 58
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Db 251 MSDWLTFFQKHINTRDVDCDNIMSTNLF---HCKDKNTFIYSRPFVKAICKGIASK 306

QY 59 NVLSTTRFQNLCTRTSITPRPCPSYSRRTETNYICVKCENQYVHFAGIGRC 110
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 307 NVLTTFEFLSDC---NVTSRPCKYKLRKSTNKFVCVCENQAPVHFVGVGSC 355

RESULT 8
US-08-875-811-57
; Sequence 57, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; APPLICATION NUMBER: US 60/011,800

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[illegible]

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/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FEATURE:
/ NAME/KEY: Protein
/ LOCATION: 1..111
/ OTHER INFORMATION: /note= "Frog Lectin from Rana
/ OTHER INFORMATION: catesbeiana"
US-08-891-848-12

Query Match          96.8%; Score 586.5; DB 2; Length 111;
Best Local Similarity 99.1%; Pred. No. 1.9e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 3 NWATFOQKHIIINPPII-CNTIMDNIIYVGQCKRVNTFIISATTVKAICTGVINNNVL 61
Db 2 NWATFOQKHIIINPPII-CNTIMDNIIYVGQCKRVNTFIISATTVKAICTGVINNNVL 61

QY 62 STTRFQINTCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRCP 111
Db 62 STTRFQINTCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRCP 111

RESULT 2
US-08-875-811-8
; Sequence 8, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..111
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/
/ OTHER INFORMATION: /note= "Frog Lectin from Rana
/ OTHER INFORMATION: catesbeiana"
US-08-875-811-8

Query Match          96.8%; Score 586.5; DB 3; Length 111;
Best Local Similarity 99.1%; Pred. No. 1.9e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 3 NWATFOQKHIIINPPII-CNTIMDNIIYVGQCKRVNTFIISATTVKAICTGVINNNVL 61
Db 2 NWATFOQKHIIINPPII-CNTIMDNIIYVGQCKRVNTFIISATTVKAICTGVINNNVL 61

QY 62 STTRFQINTCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRCP 111
Db 62 STTRFQINTCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRCP 111

RESULT 3
US-08-467-955-2
; Sequence 2, Application US/08467955
; Patent No. 5728805
; GENERAL INFORMATION:
; APPLICANT: Ardelt Ph.D, Wojciech J.
; TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark H. Jay, P.A.
; STREET: P.O. Box E
; CITY: Short Hills
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07078-0383
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,955
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/178,118
; FILING DATE: 06-APR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/436,141
; FILING DATE: 13-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,332
; FILING DATE: 03-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,970
; FILING DATE: 01-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jay, Mark H.
; REGISTRATION NUMBER: 27507
; REFERENCE/DOCKET NUMBER: 5007 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-912-9066
; TELEFAX: 201-912-0442
; TELEX: No. 5728805 Applicable
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Rana pipiens
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 11, 2004, 14:33:03 ; Search time 16.5747 Seconds  
(without alignments)  
345.738 Million cell updates/sec

Title: US-09-961-400-26

Perfect score: 606

Sequence: 1 MSNWATFOQKHINTPIICN.....ICVKCENQYPVHFAGIGRCP 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/2/iaa/5A-COMB.pep:\*
- 2: /cgn2\_6/ptodata/2/iaa/5B-COMB.pep:\*
- 3: /cgn2\_6/ptodata/2/iaa/5A-COMB.pep:\*
- 4: /cgn2\_6/ptodata/2/iaa/5B-COMB.pep:\*
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- 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	586.5	96.8	111	2	US-08-891-848-12
2	586.5	96.8	111	3	US-08-875-811-8
3	282.5	46.6	104	1	US-08-467-955-2
4	281.5	46.5	112	3	US-08-875-811-32
5	281.5	46.5	251	3	US-08-875-811-59
6	281.5	46.5	254	3	US-08-875-811-61
7	281.5	46.5	355	3	US-08-875-811-49
8	281.5	46.5	355	3	US-08-875-811-57
9	281.5	46.5	355	3	US-08-875-811-64
10	281.5	46.5	366	3	US-08-875-811-55
11	277.5	45.8	105	3	US-08-875-811-39
12	277.5	45.8	355	3	US-08-875-811-41
13	277.5	45.8	358	3	US-08-875-811-51
14	276.5	45.6	105	3	US-08-875-811-26
15	272.5	45.0	104	1	US-08-283-971-1
16	272.5	45.0	104	1	US-07-921-619-1
17	272.5	45.0	104	1	US-08-467-955-1
18	272.5	45.0	104	2	US-08-891-848-13
19	272.5	45.0	104	3	US-08-875-811-1
20	272.5	45.0	104	3	US-09-394-268-1
21	272.5	45.0	104	4	US-09-071-672-1
22	272.5	45.0	104	4	US-09-687-748-1
23	272.5	45.0	104	4	US-08-626-288-1
24	272.5	45.0	104	4	US-09-095-429-1
25	272.5	45.0	104	4	US-09-986-119-1
26	272.5	45.0	106	3	US-08-875-811-28
27	272.5	45.0	107	3	US-08-875-811-30

28	272.5	45.0	129	3	US-08-875-811-63
29	272.5	45.0	358	3	US-08-875-811-45
30	272.5	45.0	365	3	US-08-875-811-53
31	272.5	45.0	379	3	US-08-875-811-43
32	270.5	44.6	105	3	US-08-875-811-24
33	269.5	44.5	104	4	US-08-626-288-2
34	269.5	44.5	104	4	US-09-095-429-2
35	267.5	44.1	104	3	US-09-394-268-2
36	267.5	44.1	104	4	US-09-687-748-2
37	254.5	42.0	107	3	US-08-875-811-20
38	239.5	39.5	111	3	US-08-875-811-22
39	236.5	39.0	360	3	US-08-875-811-47
40	235	38.8	114	3	US-09-223-118-3
41	226	37.3	114	3	US-09-223-118-2
42	225	37.1	114	3	US-09-223-118-1
43	224	37.0	114	3	US-09-223-118-4
44	206	34.0	83	3	US-08-875-811-2
45	206	34.0	83	4	US-09-071-672-3

#### ALIGNMENTS

#### RESULT 1

US-08-891-848-12  
; Sequence 12, Application US/08891848  
; Patent No. 5955073  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Youle, Richard J.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: Nicholls, Peter J.  
; TITLE OF INVENTION: Selective RNase Cytotoxic Reagents  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/891,848  
; FILING DATE: NO. 5955073 yet assigned  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/125,462  
; FILING DATE: 22-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/014,082  
; FILING DATE: 04-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/779,195  
; FILING DATE: 22-OCT-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/510,696  
; FILING DATE: 20-APR-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 015280-110310US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 111 amino acids  
; TYPE: amino acid

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QY 34 CKRVNTFIISATVKAICTG-----VINNVLTSTRFQNTCTRTSTTPR-PCPYSSRTE 88
| | | | | : | | | | : | | | | : | | | | : | | | | :
Db 39 CKEVNTFIHTRNDIKAICNDKNGEPYNFRSRKSPFOITTCRKHGGSNRPPOGGRATAG 98
| | | | | : | | | | : | | | | : | | | | : | | | | :
QY 89 TNYICVKCENQYPVHF 104
| | | | | : | | | | : | | | | : | | | | :
Db 99 FRTIACENGLPVHF 114
| | | | | : | | | | : | | | | : | | | | :

RESULT 15
NRGPB
pancreatic ribonuclease (EC 3.1.1.27.5) B - guinea pig (tentative sequence)
N;Alternate names: RNase IB
C;Species: Cavia porcellus (guinea pig)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Accession: A00826
R;van den Berg, A.; van den Hende-Timmer, L.; Hofsteenge, J.; Gastra, W.; Beintema, J.J.
Eur. J. Biochem. 75, 91-100, 1977
A;Title: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structure a
A;Reference number: A91247; MUID:77185023; PMID:862624
A;Accession: A00826
A;Molecule type: protein
A;Residues: 1-128 <VAN>
A;Note: 64-Pro was also found
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;21,34/Binding site: carbohydrate (asn) (covalent) #status experimental
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

Query Match 19.6%; Score 118.5; DB 1; Length 128;
Best Local Similarity 31.6%; Pred. No. 8.7e-05;
Matches 37; Conservative 14; Mismatches 43; Indels 23; Gaps 6;

QY 7 FQKH-----INTPLICIMDNNIYVGGQCKRVNTFIISATVKAICTGVINNV 60
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Db 8 FQRQMDPEGSPSSNVCNMVMIIR-NMTQGRCKPVNTFVHESLADYQAVC---FQKNV 63
| | | | : | | | : | | | | : | | | | : | | | | :
QY 61 L-----STRFQNTCTRTSTTPR-CPYSSRTEINYICVKENQ--YPVHF 104
| | | | : | | | : | | | | : | | | | : | | | | :
Db 64 LCKNGQTCYQSYSRMITDCRVTSKSKFPCNCSYRMSQAQKSIIVACEGDPYVPVHF 120
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Job time : 13.5611 secs





Db 6 AKFERQHIDNPSSVSSNNYCNQMMKSR-NLTQGRCKPVNTFVHESLADVAVCS---QK 61  
QY 59 NVL-----STTRFQLNCTRTSITPRP-CPYSSRTETNYICVKCE-NOY-PVHF 104  
Db 62 NVACKNGQNCYQSYSTMSITDCRETGSSKYPNCAKTKQAKHIIIVACBGNPYVPVHY 120  
RESULT 11  
NRKGR  
pancreatic ribonuclease (EC 3.1.1.27.5) - red kangaroo  
N/Alternate names: RNase 1; RNase A  
C/Species: Macropus rufus, Megalera rufa (red kangaroo)  
C/Date: 30-Nov-1980 #sequence\_revision 30-Nov-1980 #text\_change 04-Oct-1996  
C/Accession: A00833  
R/Gaaster, W.; Wellington, G.W.; Beintema, J.J.  
A/Title: The amino-acid sequence of kangaroo pancreatic ribonuclease.  
A/Reference number: A00833; MUID:78190621; PMID:659039  
A/Accession: A00833  
A/Molecule type: protein  
A/Residues: 1-122 <GAA>  
C/Superfamily: pancreatic ribonuclease  
C/Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
F/11,40,117/Active site: His, Lys, His #status predicted  
F/25-83,39-94,57-109,64-71/Disulfide bonds: #status predicted  
F/61/Binding site: carbohydrate (Asn) (covalent) #status absent  
Query Match 20.1%; Score 122; DB 1; Length 122;  
Best Local Similarity 30.7%; Pred. No. 3.7e-05;  
Matches 35; Conservative 16; Mismatches 45; Indels 18; Gaps 6;  
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Db 7 FQGHMDTEHSTASSNYCNLMKAR-DMTSGRCKPLNTHPEKSVDAVCHQENVTCK 65  
QY 53 TGVNNVLTTRFQLNCTRTSITPRP-CPYSSRTETNYICVKCE-NOY-PVHF 104  
Db 66 NGRNLC-YKSNRLSITNCRQTGASKYPNCQYETSNLKQIIVACBGNPYVPVHF 118  
RESULT 12  
NRUC  
pancreatic ribonuclease (EC 3.1.1.27.5) - nutria (tentative sequence)  
N/Alternate names: RNase 1; RNase A  
C/Species: Myocastor coypus (nutria, coypu)  
C/Date: 24-Apr-1984 #sequence\_revision 30-Sep-1988 #text\_change 31-Mar-2000  
C/Accession: A00822  
R/van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.  
Biochim. Biophys. Acta 453, 400-409, 1976  
A/Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic  
A/Reference number: A00822; MUID:77065676; PMID:999896  
A/Accession: A00822  
A/Molecule type: protein  
A/Residues: 1-128 <VAN>  
C/Superfamily: pancreatic ribonuclease  
C/Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
F/12,41,119/Active site: His, Lys, His #status predicted  
F/26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted  
F/34/Binding site: carbohydrate (Asn) (covalent) #status experimental  
Query Match 19.9%; Score 120.5; DB 1; Length 128;  
Best Local Similarity 31.6%; Pred. No. 5.5e-05;  
Matches 37; Conservative 15; Mismatches 42; Indels 23; Gaps 7;  
QY 7 FQOKHI-----INTPIICNTIMNNIYIVGGCKRVNTFISSATVKAICGVINMV 60  
Db 8 FERQHDMSRGSPTSNYCNEMKSR-NMTQGRCKPVNTFVHESLADVAVCS---FQKNV 63  
QY 61 L-----STTRFQLNCTRTSITPRP-CPYSSRTETNYICVKCE-NOY-PVHF 104  
Db 64 LCKNGQNCYQSNMHIITDCRTSNDYCNCSYRSQEKSIIVACBGNPYVPVHF 120

RESULT 13  
NRMS  
pancreatic ribonuclease (EC 3.1.1.27.5) precursor - mouse  
N/Alternate names: RNase 1; RNase A  
C/Species: Mus musculus (house mouse)  
C/Date: 30-Nov-1980 #sequence\_revision 13-Mar-1997 #text\_change 18-Jun-1999  
C/Accession: A34090; S22598; A00830  
R/Schueler, C.; Nijssen, H.M.J.; Kok, R.; Beintema, J.J.  
Mol. Biol. Evol. 7, 29-44, 1990  
A/Title: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of mouse  
A/Reference number: A34090; MUID:90136034; PMID:2299980  
A/Accession: A34090  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-149 <SCH>  
A/Cross-references: GB:M27814; NID:G200762; PIDN:AAA40060.1; PID:G200763  
R/Samuelson, L.C.; Wiebauer, K.; Howard, G.; Schmid, R.M.; Koeplin, D.; Meisler, M.H.  
Nucleic Acids Res. 19, 6935-6941, 1991  
A/Title: Isolation of the murine ribonuclease gene Rib-1: structure and tissue specific  
A/Reference number: S22598; MUID:92107684; PMID:1840677  
A/Accession: S22598  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-149 <SAM>  
A/Cross-references: EMBL:X60103; NID:G53981; PIDN:CAA42697.1; PID:G53982  
R/Lenstra, J.A.; Beintema, J.J.  
Eur. J. Biochem. 98, 399-408, 1979  
A/Title: The amino acid sequence of mouse pancreatic ribonuclease.  
A/Reference number: A00830; MUID:80024269; PMID:556267  
A/Accession: A00830  
A/Molecule type: protein  
A/Residues: 26-149 <LEN>  
C/Superfamily: pancreatic ribonuclease  
C/Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
F/1-25/Domain: signal sequence #status predicted <SIG>  
F/26-149/Product: pancreatic ribonuclease #status experimental <MAT>  
F/37,66,144/Active site: His, Lys, His #status predicted  
F/51-109,65-120,83-135,90-97/Disulfide bonds: #status predicted  
F/62,87/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 19.9%; Score 120.5; DB 1; Length 149;  
Best Local Similarity 30.8%; Pred. No. 6.5e-05;  
Matches 36; Conservative 16; Mismatches 42; Indels 23; Gaps 7;  
QY 7 FQOKHI-----INTPIICNTIMNNIYIVGGCKRVNTFISSATVKAICGVINMV 60  
Db 33 FQGHMDPDGSSINSPTCYNQMKRR-DMTNGSCKPVNTFVHESLADVAVCS---QENV 88  
QY 61 L-----STTRFQLNCTRTSITPRP-CPYSSRTETNYICVKCE-NOY-PVHF 104  
Db 89 TCKNRKSNCKYSSSALHITDCHLKGNSKYPNCYKTKTQYQKHIIIVACBGNPYVPVHF 145  
RESULT 14  
A43825  
angiogenin - pig  
C/Species: Sus scrofa domestica (domestic pig)  
C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C/Accession: S29834; A43825  
R/Bond, M.D.; Strydom, D.J.; Vallee, B.L.  
Biochim. Biophys. Acta 1162, 177-186, 1993  
A/Title: Characterization and sequencing of rabbit, pig and mouse angiogenins: discernmer  
A/Reference number: S29833; MUID:93192291; PMID:8448182  
A/Accession: S29834  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-123 <BON>  
A/Note: this sequence was submitted to the Protein Sequence Database, December 1992  
C/Superfamily: pancreatic ribonuclease  
Query Match 19.7%; Score 119.5; DB 1; Length 123;  
Best Local Similarity 39.5%; Pred. No. 6.7e-05;  
Matches 30; Conservative 6; Mismatches 35; Indels 5; Gaps 2;

S20066  
pancreatic-type ribonuclease (EC 3.1.1.27.5) BRB precursor, brain - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 22-Nov-1993 #sequence\_revision 12-May-1995 #text\_change 22-Jun-1999  
C:Accession: S20066; JX0056  
R:Sasano, M.P.; Carsana, A.; Confalone, E.; Cosi, C.; Sorrentino, S.; Viola, M.; Palmieri  
Nucleic Acids Res. 19, 6469-6474, 1991  
A:Title: Molecular cloning of the gene encoding the bovine brain ribonuclease and its ex  
A:Reference number: S20066; MUID:92093604; PMID:1754384  
A:Accession: S20066  
A:Molecule type: DNA  
A:Residues: 1-167 <SAS>  
A:Cross-references: EMBL:X59767; NID:gl50; PIDN:CAA42439.1; PID:gl51  
R:Watanabe, H.; Katoh, H.; Ishii, M.; Komoda, Y.; Sanda, A.; Takizawa, Y.; Ohgi, K.; Iri  
J. Biochem. 104, 939-945, 1988  
A:Title: Primary structure of a ribonuclease from bovine brain.  
A:Reference number: JX0056; MUID:89214015; PMID:3243767  
A:Accession: JX0056  
A:Molecule type: protein  
A:Residues: 27-154, 'S', 156-166 <WAT>  
A:Experimental source: brain  
C:Superfamily: pancreatic ribonuclease  
C:Keywords: glycoprotein; hydrolase  
F:38,67,145/Active site: His, Lys, His #status predicted  
F:52-110,66-121,84-136,91-98/Disulfide bonds: #status predicted  
F:88/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:155/Binding site: carbohydrate (Thr) (covalent) #status experimental  
F:159/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 22.0%; Score 133.5; DB 2; Length 167;  
Best Local Similarity 31.4%; Pred. No. 3.7e-06;  
Matches 38; Conservative 17; Mismatches 43; Indels 23; Gaps 7;

QY 5 ATFOQKH-----INTPLICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVNM 58  
DB 32 AKFREQHMDSGSSSNPNYCNQMRR-RWTHGRCKPVNTFVHESLDVKAICS---QK 87  
QY 59 NVL-----STTRFQLNCTRTSITPRP-CPYSSRTETNYICVCKE-NOY-PVHFA 105  
DB 88 NITCKNGHPNCVQSTWSITDCRTGSGKYENCAYKTSQKQYITVACEGPPVPHFD 147  
QY 106 G 106  
DB 148 G 148

RESULT 8  
NRPG  
pancreatic ribonuclease (EC 3.1.1.27.5) - pig  
N:Alternate names: RNase A  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 03-Jun-1994  
C:Accession: A92071; A91391; A00816  
R:Jackson, R.L.; Hirs, C.H.W.  
J. Biol. Chem. 245, 637-653, 1970  
A:Title: The primary structure of porcine pancreatic ribonuclease. II. The amino acid se  
A:Reference number: A92071; MUID:70104197; PMID:5460946  
A:Accession: A92071  
A:Molecule type: protein  
A:Residues: 1, 'Q', 3-124 <JAC>  
R:Wierenga, R.K.; Huijzinga, J.D.; Gaastera, W.; Welling, G.W.; Beintema, J.J.  
FEBS Lett. 31, 181-185, 1973  
A:Title: Affinity chromatography of porcine pancreatic ribonuclease and reinvestigation  
A:Reference number: A91391  
A:Accession: A91391  
A:Molecule type: protein  
A:Residues: 1-124 <WIE>  
R:Phelan, J.J.; Hirs, C.H.W.  
J. Biol. Chem. 245, 654-661, 1970  
A:Title: The primary structure of porcine pancreatic ribonuclease. III. The disulfide bo  
A:Reference number: A92072; MUID:70104198; PMID:4904878  
A:Contents: annotation; disulfide bonds  
C:Superfamily: pancreatic ribonuclease

C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
F:12,41,119/Active site: His, Lys, His #status predicted  
F:21,34,76/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status experimental

Query Match 21.9%; Score 132.5; DB 1; Length 124;  
Best Local Similarity 31.6%; Pred. No. 3.4e-06;  
Matches 36; Conservative 19; Mismatches 42; Indels 17; Gaps 6;

QY 7 FQCKHI-----INTPLICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGV-INNM 59  
DB 8 FORQHMDDSSSNPNYCNQMRR-NMTQGRCKPVNTFVHESLDVKAICSQINNVCK 66  
QY 60 VLSTTRFQLNCTRTSITPRP-CPYSSRTETNYICVCKENQ--YPVHF 104  
DB 67 NGQTCYQSNIMHITDCRGTGSSKYPNCAYKASQEQKHIIIVACEGNPPVPHF 120

RESULT 9  
S4111  
pancreatic ribonuclease - common iguana  
C:Species: Iguana iguana (common iguana)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 21-Aug-1998  
C:Accession: S4111  
R:Zhao, W.; Beintema, J.J.; Hofsteenge, J.  
Eur. J. Biochem. 219, 641-646, 1994  
A:Title: The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease.  
A:Reference number: S4111; MUID:94139745; PMID:9307028  
A:Accession: S4111  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-119 <ZHA>  
C:Superfamily: pancreatic ribonuclease

Query Match 20.9%; Score 126.5; DB 2; Length 119;  
Best Local Similarity 29.8%; Pred. No. 1.3e-05;  
Matches 34; Conservative 16; Mismatches 51; Indels 13; Gaps 4;

QY 3 NWATFQKH-----INTPLICNTIMDNNIYVGGCKRVNTFISSATTVKAIC--- 52  
DB 2 DWSSFQKHIDYPTASNPAYCDLMMQRR-NLNPTRCKTRNTFVHASEIQVGGSG 60  
QY 53 -TGVINMNVLTTRFQLNCTRTSIT-PRPCPYSSRTETNYICVCKENQYPVHF 104  
DB 61 GTHYEDNLYDSNESFDLTDCKNVGTFAPSSCKYNGTPTGKRIRIACENQPVHF 114

RESULT 10  
NRPRH  
pancreatic ribonuclease (EC 3.1.1.27.5) - pronghorn (tentative sequence)  
N:Alternate names: RNase 1; RNase A  
C:Species: Antilocapra americana (pronghorn)  
C:Date: 28-Feb-1981 #sequence\_revision 28-Feb-1981 #text\_change 31-Mar-2000  
C:Accession: A00813  
R:Beintema, J.J.; Gaastera, W.; Munnikma, J.  
J. Mol. Evol. 13, 305-316, 1979  
A:Title: Primary structure of pronghorn pancreatic ribonuclease: close relationship bew  
A:Reference number: A00813; MUID:80075014; PMID:513141  
A:Accession: A00813  
A:Molecule type: protein  
A:Residues: 1-124 <BEI>  
C:Superfamily: pancreatic ribonuclease  
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
F:12,41,119/Active site: His, Lys, His #status predicted  
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted  
F:34/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 20.2%; Score 122.5; DB 1; Length 124;  
Best Local Similarity 30.3%; Pred. No. 3.4e-05;  
Matches 36; Conservative 18; Mismatches 42; Indels 23; Gaps 7;

QY 5 ATFOQKHINTPI-----ICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVNM 58  
DB 119 G 119

## RESULT 7

Result No.	Score	Query Match	length	ID	Description
1	586.5	96.8	111	2	A27121
2	450	74.3	111	1	JX00120
3	369	60.9	111	2	UX0085
4	272.5	45.0	104	2	A39035
5	135.5	22.4	124	1	NRWHK
6	135.5	22.4	145	1	A35932
7	133.5	22.0	167	2	S20066
8	132.5	21.9	124	1	NRPG
9	126.5	20.9	119	2	S41111
10	122.5	20.2	124	1	NRPRH
11	122	20.1	122	1	NRKGR
12	120.5	19.5	128	1	NRCU
13	120.5	19.9	149	1	NRMS
14	119.5	19.7	123	1	A43825
15	118.5	19.6	128	1	NRGPB
16	117.5	19.4	128	1	NRHO
17	116.5	19.2	124	1	NRCM
18	116.5	19.2	124	1	NRCMM
19	116.5	19.2	124	1	NRCMB
20	116.5	19.2	128	1	NRKS
21	114.5	18.9	124	2	S08549
22	114	18.8	125	1	A32474
23	113.5	18.7	124	1	NRDEN
24	113.5	18.7	125	1	B43825
25	113	18.6	147	1	NRUDAG
26	112.5	18.6	124	1	NRGE
27	112.5	18.6	124	1	NRDEO
28	111.5	18.4	130	2	S22808
29	110.5	18.2	124	1	NRBOB
30	110.5	18.2	124	1	NRBOB
31	110.5	18.2	124	1	NRBOB
32	110.5	18.2	124	1	NRBOB
33	110.5	18.2	124	1	NRBOB
34	110.5	18.2	124	1	NRBOB
35	110.5	18.2	124	1	NRBOB
36	110.5	18.2	124	1	NRBOB
37	110.5	18.2	124	1	NRBOB
38	110.5	18.2	124	1	NRBOB
39	110.5	18.2	124	1	NRBOB
40	110.5	18.2	124	1	NRBOB
41	110.5	18.2	124	1	NRBOB
42	110.5	18.2	124	1	NRBOB
43	110.5	18.2	124	1	NRBOB
44	110.5	18.2	124	1	NRBOB
45	110.5	18.2	124	1	NRBOB
46	110.5	18.2	124	1	NRBOB
47	110.5	18.2	124	1	NRBOB
48	110.5	18.2	124	1	NRBOB
49	110.5	18.2	124	1	NRBOB
50	110.5	18.2	124	1	NRBOB
51	110.5	18.2	124	1	NRBOB
52	110.5	18.2	124	1	NRBOB
53	110.5	18.2	124	1	NRBOB
54	110.5	18.2	124	1	NRBOB
55	110.5	18.2	124	1	NRBOB
56	110.5	18.2	124	1	NRBOB
57	110.5	18.2	124	1	NRBOB
58	110.5	18.2	124	1	NRBOB
59	110.5	18.2	124	1	NRBOB
60	110.5	18.2	124	1	NRBOB
61	110.5	18.2	124	1	NRBOB
62	110.5	18.2	124	1	NRBOB
63	110.5	18.2	124	1	NRBOB
64	110.5	18.2	124	1	NRBOB
65	110.5	18.2	124	1	NRBOB
66	110.5	18.2	124	1	NRBOB
67	110.5	18.2	124	1	NRBOB
68	110.5	18.2	124	1	NRBOB
69	110.5	18.2	124	1	NRBOB
70	110.5	18.2	124	1	NRBOB
71	110.5	18.2	124	1	NRBOB
72	110.5	18.2	124	1	NRBOB
73	110.5	18.2	124	1	NRBOB
74	110.5	18.2	124	1	NRBOB
75	110.5	18.2	124	1	NRBOB
76	110.5	18.2	124	1	NRBOB
77	110				



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OS Rana pipiens.
OS Synthetic.
XX WO9731116-A2.
XX PD 28-AUG-1997.
XX PF 19-FEB-1997; 97WO-US002588.
XX PR 21-FEB-1996; 96US-0011800P.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Rybak SM, Newton DL, Boque L, Wlodawer A;
XX WPI; 1997-435168/40.
XX DR N-PSDB; AAT94972.
XX RI Ribonuclease molecules based on native Onconase - used for killing cells,
XX PT particularly tumour cells.
XX PS Disclosure; Page 76; 90pp; English.
XX CC Sequences AAW35125 to AAW35135 represent recombinant fusion proteins
XX (rOnc) which are modifications of the RNase Onconase (RTM) (nOnc). Such
XX novel ribonuclease molecules are highly cytotoxic and can be used alone
XX or to form chemical conjugates or to target recombinant immunofusions.
XX They are used particularly for decreasing tumour cell growth. They can
XX also be used for cell separation in vitro by selectively killing unwanted
XX patient undergoing marrow ablation by radiation, or for killing leukaemia
XX cells or T-cells that would cause graft versus host disease. The toxins
XX can also be used to selectively kill unwanted cells in culture. The new
XX ribonucleases have increased cytotoxic activity compared to nOnc and also
XX lower immunogenicity in humans
XX SQ Sequence 251 AA;
XX
XX Query Match 46.5%; Score 281.5; DB 2; Length 251;
XX Best Local Similarity 50.0%; Pred. NO. 8.7e-24;
XX Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
XX
QY 1 MSNWATFOOKHIINT-PIICNTIMDNNIYVGQCKRVNTFISSATTVKAICTGVI-NM 58
DB 147 MSDWLTFFQKKHITNRDVCDDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGLIASK 202
XX
QY 59 NVLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCNQYVPHFAGIGRC 110
DB 203 NVLTTFEYFLSDC---NVTSRPCKYKLLKSTNKFCVTCENQAPVHFVGVGSC 251
XX
RESULT 13
AAW35135
ID AAW35135 standard; protein; 254 AA.
XX
AC AAW35135;
XX
XX 20-APR-1998 (first entry)
XX
DE R. pipiens recombinant RNase rOnc fusion protein 11.
XX
XX RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
XX tumour cell growth; frog.
XX
XX Rana pipiens.
XX OS Synthetic.
XX WO9731116-A2.
XX PD 28-AUG-1997.
XX PF 19-FEB-1997; 97WO-US002588.
XX PR 21-FEB-1996; 96US-0011800P.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Rybak SM, Newton DL, Boque L, Wlodawer A;
XX WPI; 1997-435168/40.
XX DR N-PSDB; AAT94972.
XX RI Ribonuclease molecules based on native Onconase - used for killing cells,
XX PT particularly tumour cells.
XX PS Disclosure; Page 76; 90pp; English.
XX CC Sequences AAW35125 to AAW35135 represent recombinant fusion proteins
XX (rOnc) which are modifications of the RNase Onconase (RTM) (nOnc). Such
XX novel ribonuclease molecules are highly cytotoxic and can be used alone
XX or to form chemical conjugates or to target recombinant immunofusions.
XX They are used particularly for decreasing tumour cell growth. They can
XX also be used for cell separation in vitro by selectively killing unwanted
XX patient undergoing marrow ablation by radiation, or for killing leukaemia
XX cells or T-cells that would cause graft versus host disease. The toxins
XX can also be used to selectively kill unwanted cells in culture. The new
XX ribonucleases have increased cytotoxic activity compared to nOnc and also
XX lower immunogenicity in humans
XX SQ Sequence 254 AA;
XX
XX Query Match 46.5%; Score 281.5; DB 2; Length 254;
XX Best Local Similarity 50.0%; Pred. NO. 8.8e-24;
XX Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
XX
QY 1 MSNWATFOOKHIINT-PIICNTIMDNNIYVGQCKRVNTFISSATTVKAICTGVI-NM 58
DB 1 MSDWLTFFQKKHITNRDVCDDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGLIASK 56
XX
QY 59 NVLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCNQYVPHFAGIGRC 110
DB 57 NVLTTFEYFLSDC---NVTSRPCKYKLLKSTNKFCVTCENQAPVHFVGVGSC 105
XX
RESULT 14
AAW35133
ID AAW35133 standard; protein; 355 AA.
XX
AC AAW35133;
XX
XX 20-APR-1998 (first entry)
XX
DE R. pipiens recombinant RNase rOnc fusion protein 9.
XX
XX RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
XX tumour cell growth; frog.
XX
XX Rana pipiens.
XX OS Synthetic.
XX WO9731116-A2.
XX PD 28-AUG-1997.
XX PF 19-FEB-1997; 97WO-US002588.
XX PR 21-FEB-1996; 96US-0011800P.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Rybak SM, Newton DL, Boque L, Wlodawer A;
XX WPI; 1997-435168/40.
XX DR N-PSDB; AAT94972.
XX

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RESULT 10
AAAY28867
ID AAY28867 standard; protein; 105 AA.
XX AC AAY28867;
XX 25-JAN-2000 (first entry)
XX DE Recombinant Met(-1) RaPLR1.
XX KW Recombinant Met(-1) Rana pipiens ribonuclease; RaPLR1; CD22; RNase;
XX covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
XX Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;
XX recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
XX autoimmune disease.
XX OS Rana pipiens.
XX OS Synthetic.
XX Key Location/Qualifiers
FT Misc-difference 1 /note= "Met not found in wild type RaPLR1"
FT
XX PN WO9950398-A2.
XX PD 07-OCT-1999.
XX XX 26-MAR-1999; 99WO-US006641.
XX PF 27-MAR-1998; 98US-0079751P.
XX PR
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Rybak SM, Newton DL;
XX XX WPI; 1999-610847/52.
XX DR N-PSDE; AAZ08126.
XX PT New recombinant ribonucleases, used for killing target cells, e.g. for
XX treating cancers, viral infections or autoimmune diseases.
XX PS Claim 34; Page 57; 71pp; English.
XX CC The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1)
XX protein with Met at position 1. Carboxy terminal end of recombinant
XX RaPLR1 has a covalently bound ligand binding moiety, which can be a LL2
XX antibody directed against CD22 on cancerous B cells or human chorionic
XX gonadotropin (hCG) effective against Kaposi's sarcoma cells. Recombinant
XX ribonucleases can be expressed in bacteria without an N-terminal
XX methionine due to the presence of a signal peptide that is cleaved by
XX bacteria. The soluble expression of ribonuclease allows the proteins to
XX be fused in-frame with ligand binding moieties to form cytotoxic fusion
XX proteins. They can be used for treatment of cancer and autoimmune
XX diseases
XX SQ Sequence 105 AA;
Query Match 46.5%; Score 281.5; DB 2; Length 105;
Best Local Similarity 49.1%; Pred. No. 2.9e-24;
Matches 55; Conservative 15; Mismatches 33; Indels 9; Gaps 4;
Qy 1 MSNWATFOQKHINT-PIICNTIMDNNIYVGGCKRVNTFISSATTVAICTGVI-NM 58
Db 1 MQDWLTFQKKHLTNRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASK 56
Qy 59 NVLSTTRFQNLTCRTISITRPPCPYSRTEITNYICVKCENQYVHFAGIGRC 110
Db 57 NVLTTSEFYLSDC---NVTSRPCKYKLKSTNFCVTCENQAPVHFVGVGHC 105
RESULT 11
AAW35118
ID AAW35118 standard; protein; 112 AA.
XX AC AAW35118;
XX 20-APR-1998 (first entry)
XX DE R. pipiens recombinant RNase protein NLSMetSerrOnc.
XX KW RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
XX tumour cell growth; frog.
XX OS Rana pipiens.
XX PN WO9731116-A2.
XX PD 28-AUG-1997.
XX PF 19-FEB-1997; 97WO-US002588.
XX PR 21-FEB-1996; 96US-0011800P.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Rybak SM, Newton DL, Boque L, Wlodawer A;
XX XX WPI; 1997-435168/40.
XX DR N-PSDE; AAT94955.
XX PT Ribonuclease molecules based on native Onconase - used for killing cells,
XX particularly tumour cells.
XX PS Claim 18; Page 63; 90pp; English.
XX CC AAW35115 to AAW35123 encode recombinant proteins (rOnc) which are
XX modifications of the RNase Onconase (RTM) (nOnc). Such novel ribonuclease
XX molecules are highly cytotoxic and can be used alone or to form chemical
XX conjugates or to target recombinant immunofusions. They are used
XX particularly for decreasing tumour cell growth. They can also be used for
XX cell separation in vitro by selectively killing unwanted types of cells,
XX e.g. in bone marrow prior to transplantation into a patient undergoing
XX marrow ablation by radiation, or for killing leukaemia cells or T-cells
XX that would cause graft versus host disease. The toxins can also be used
XX to selectively kill unwanted cells in culture. The new ribonucleases have
XX increased cytotoxic activity compared to nOnc and also lower
XX immunogenicity in humans
XX SQ Sequence 112 AA;
Query Match 46.5%; Score 281.5; DB 2; Length 112;
Best Local Similarity 50.0%; Pred. No. 3.2e-24;
Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
Qy 1 MSNWATFOQKHINT-PIICNTIMDNNIYVGGCKRVNTFISSATTVAICTGVI-NM 58
Db 8 MSDWLTFQKKHLTNRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASK 63
Qy 59 NVLSTTRFQNLTCRTISITRPPCPYSRTEITNYICVKCENQYVHFAGIGRC 110
Db 64 NVLTTSEFYLSDC---NVTSRPCKYKLKSTNFCVTCENQAPVHFVGVGSC 112
RESULT 12
AAW35134
ID AAW35134 standard; protein; 251 AA.
XX AC AAW35134;
XX 20-APR-1998 (first entry)
XX DE R. pipiens recombinant RNase rOnc fusion protein 10.
XX KW RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
XX tumour cell growth; frog.
XX XX

```

CC (Rana catesbeiana) lectin used to describe the method of the invention

XX Sequence 111 AA;

SQ Query Match 96.8%; Score 586.5; DB 2; Length 111;

Best Local Similarity 99.1%; Pred. NO. 3.6e-59;

Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 3 NWATFOQKHINTPII-CNTIMDNNIYVGGQCKRVNTFISSATVKAICTGVINNMVL 61

DB 2 NWATFOQKHINTPIINCNTIMDNNIYVGGQCKRVNTFISSATVKAICTGVINNMVL 61

QY 62 STTRFQNLNCTRTSITPRCPYSSRTETNYICVKCENQYVHFAGIGRCP 111

DB 62 STTRFQNLNCTRTSITPRCPYSSRTETNYICVKCENQYVHFAGIGRCP 111

RESULT 8

AAV28871

ID AAY28871 standard; protein; 105 AA.

XX AC AAY28871;

XX 25-JAN-2000 (first entry)

DT Recombinant Met(-1) RaPLR1 Gln1Ser amino acid sequence.

DE

XX Recombinant Met(-1) Rana pipiens ribonuclease Gln1Ser; RaPLR1; CD22;

KW covalently bound; IL2 antibody; ligand binding moiety; cancerous B cell;

KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;

KW recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;

KW autoimmune disease; RNase.

XX

OS Rana pipiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 1 /note= "Met not found in wild type RaPLR1"

FT Misc-difference 2 /note= "Wild type Gln replaced with Ser"

FT

FN WO9950398-A2.

XX

PD 07-OCT-1999.

XX

PF 26-MAR-1999; 99WO-US006641.

XX

PR 27-MAR-1998; 98US-0079751P.

XX

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Rybak SM, Newton DL;

PI WPI; 1999-610847/52.

XX DR N-PSDB; AA208129.

XX

PT New recombinant ribonucleases, used for killing target cells, e.g. for

PT treating cancers, viral infections or autoimmune diseases.

XX

PS Claim 34; Page 61; 71pp; English.

XX

CC The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1)

CC protein with Met at position 1 and Gln2Ser. Carboxy terminal end of

CC recombinant RaPLR1 has a covalently bound ligand binding moiety, which

CC can be a IL2 antibody directed against CD22 on cancerous B cells or human

CC chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.

CC Recombinant ribonucleases can be expressed in bacteria without an N-

CC terminal methionine due to the presence of a signal peptide that is

CC cleaved by bacteria. The soluble expression of ribonuclease allows the

CC proteins to be fused in-frame with ligand binding moieties to form

CC cytotoxic fusion proteins. They can be used for treatment of cancer and

CC autoimmune diseases

XX Sequence 105 AA;

SQ Query Match 47.1%; Score 285.5; DB 2; Length 105;

Best Local Similarity 50.0%; Pred. NO. 1e-24;

Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 MGNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATVKAICTGVI-NM 58

DB 1 MGDWLTFOQKHINTFDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASK 56

QY 59 NVLSTTRFQNLNCTRTSITPRCPYSSRTETNYICVKCENQYVHFAGIGRGC 110

DB 57 NVLTTFSEFYLSDC---NVTSRPCKYKLLKSTNFCVTCENQAPVHFVGVGHC 105

RESULT 9

AAW06544

ID AAW06544 standard; protein; 104 AA.

XX AC AAW06544;

XX 22-AUG-1997 (first entry)

DT Antitumour protein from Rana pipiens oocytes.

DE Antitumour protein from Rana pipiens oocytes.

XX Tumour; chemotherapy; radiotherapy; frog.

XX Rana pipiens.

XX WO9639428-A1.

XX 12-DEC-1996.

XX

PF 03-JUN-1996; 96WO-US008304.

XX

PR 06-JUN-1995; 95US-00467955.

XX (ALFA-) ALFACELL CORP.

XX Ardelt WJ;

XX WPI; 1997-043063/04.

XX Antitumour proteins from Rana pipiens oocyte(s) - have fewer

XX disadvantages than chemotherapy, surgery and radiotherapy.

XX Claim 8; Page 28; 45pp; English.

XX The present sequence is a specifically claimed example of an antitumour

XX protein from the generic protein in AAW18224, with the molecular weight

XX 12000. This is one of two preferred proteins (the other in AAW06543) that

XX have been isolated from Rana pipiens oocytes. Both proteins have a

XX blocked amino terminal group and are essentially free of carbohydrates.

XX The proteins are used to treat tumours. Use of the peptides has fewer

XX disadvantages than chemotherapy, radiotherapy and surgery in the

XX treatment of tumours

XX Sequence 104 AA;

SQ Query Match 46.6%; Score 282.5; DB 2; Length 104;

Best Local Similarity 50.0%; Pred. NO. 2.2e-24;

Matches 55; Conservative 15; Mismatches 31; Indels 9; Gaps 4;

QY 3 NWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATVKAICTGVI-NMNV 60

DB 2 DWTTFQKHINTFDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKNV 57

QY 61 LSTTRFQNLNCTRTSITPRCPYSSRTETNYICVKCENQYVHFAGIGRGC 110

DB 58 LITSEFYLSDC---NVTSRPCKYKLLKSTNFCVTCENQAPVHFVGVGRC 104



SQ Sequence 111 AA;  
 Query Match 98.3%; Score 596; DB 2; Length 111;  
 Best Local Similarity 97.3%; Pred. No. 3e-60;  
 Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MSNWATFOQKHIIPTICNTIMDNNIYIVGGQCKRVNTFIISATTVKAICTGVINNV 60  
 Db 1 MNWATFOQKHIIPTICNTILDNNIYIVGGQCKRVNTFIISATTVKAICTGVINLV 60  
 QY 61 LSTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111  
 Db 61 LSTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111  
 RESULT 6  
 AAY28874  
 ID AAY28874 standard; protein; 110 AA.  
 XX  
 AC AAY28874;  
 XX  
 DT 25-JAN-2000 (first entry)  
 XX  
 DE Recombinant RaCOR1 Met22Leu Met57Leu amino acid sequence.  
 XX  
 KW Recombinant Rana catesbeiana oocyte ribonuclease; covalently bound;  
 KW RaCOR1 Met22Leu Met57Leu; LL2 antibody; ligand binding moiety; CD22;  
 KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotropin; hCG;  
 KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;  
 KW cancer; bullfrog; RNase; autoimmune disease.  
 XX  
 OS Rana catesbeiana.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 22 /note= "Wild type Met replaced with Leu"  
 FT Misc-difference 57 /note= "Wild type Met replaced with Leu"  
 FT  
 XX WO9950398-A2.  
 XX  
 PD 07-OCT-1999.  
 XX  
 PF 26-MAR-1999; 99WO-US006641.  
 XX  
 PR 27-MAR-1998; 98US-0079751P.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Rybak SM, Newton DL;  
 XX  
 DR WPI; 1999-610847/52.  
 DR N-PSDB; AAZ08132.  
 XX  
 PT New recombinant ribonucleases, used for killing target cells, e.g. for  
 PT treating cancers, viral infections or autoimmune diseases.  
 XX  
 PS Claim 22; Page 64; 71pp; English.  
 XX  
 CC The present sequence is a recombinant Rana catesbeiana oocyte  
 CC ribonuclease (RaCOR1) protein with Met22Leu Met57Leu. Carboxy terminal  
 CC end of recombinant RaCOR1 has a covalently bound ligand binding moiety,  
 CC which can be a LL2 antibody directed against CD22 on cancerous B cells or  
 CC human chorionic gonadotropin (hCG) effective against Kaposi's sarcoma  
 CC cells. Recombinant ribonucleases can be expressed in bacteria without an  
 CC N-terminal methionine due to the presence of a signal peptide that is  
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the  
 CC proteins to be fused in-frame with ligand binding moieties to form  
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and  
 CC autoimmune diseases  
 XX  
 SQ Sequence 110 AA;

Query Match 97.5%; Score 591; DB 2; Length 110;  
 Best Local Similarity 98.3%; Pred. No. 1.1e-59;  
 Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 NWATFOQKHIIPTICNTIMDNNIYIVGGQCKRVNTFIISATTVKAICTGVINNVLS 62  
 Db 2 NWATFOQKHIIPTICNTILDNNIYIVGGQCKRVNTFIISATTVKAICTGVINLVLS 61  
 QY 63 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111  
 Db 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
 RESULT 7  
 AAY33321  
 ID AAY33321 standard; protein; 111 AA.  
 XX  
 AC AAY33321;  
 XX  
 DT 29-NOV-1999 (first entry)  
 XX  
 DE Frog lectin protein fragment.  
 XX  
 KW Cytotoxic; RNase; ribonuclease; pancreatic; antibody; light chain;  
 KW heavy chain; cell surface marker; treatment; tumor; viral infection;  
 KW parasite infection; immune dysfunctional cell; autoimmune disease;  
 KW contraceptive; cell separation; transplantation; bone marrow ablation;  
 KW leukemia cell; T-cell; graft-versus-host disease; bullfrog; lectin.  
 XX  
 OS Rana catesbeiana.  
 OS  
 XX US9555073-A.  
 XX  
 PD 21-SEP-1999.  
 XX  
 PF 09-JUL-1997; 97US-00891848.  
 XX  
 PR 20-APR-1990; 90US-00510696.  
 PR 22-OCT-1991; 91US-00779195.  
 PR 04-FEB-1993; 93US-00014082.  
 PR 22-SEP-1993; 93US-00125462.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Rybak SM, Newton DL, Nicholls PJ, Youle RJ;  
 XX  
 DR WPI; 1999-560488/47.  
 XX  
 PT Recombinantly fused pancreatic RNase-targeting proteins useful for  
 PT treating tumors, infections, immune or autoimmune disorders and as a  
 PT contraceptive.  
 XX  
 PS Example 3; Fig 19; 47pp; English.  
 XX  
 CC This invention describes a novel nucleic acid construct comprising  
 CC sequences encoding functional pancreatic RNase and a second protein  
 CC (preferably the light and heavy chains of an antibody) which binds a  
 CC specific cell surface marker on a target cell and functions as a  
 CC cytotoxic agent. The products can be used for selectively killing cells  
 CC expressing a specific surface marker. They can be used for treating  
 CC tumors or infected cells (e.g. cells infected by viruses (especially  
 CC latent or chronic virus infections, such as human immunodeficiency virus  
 CC (HIV)-1, Epstein-Barr virus, herpes viruses (herpes simplex types I and  
 CC II), hepatitis viruses (B, non-A non-B, and delta), herpes zoster,  
 CC cytomegalovirus) and cells infected with parasites (such as the malaria  
 CC parasite)). They can also be used for treating immune dysfunctional cells  
 CC in immune and autoimmune diseases. Additionally, they may be used as  
 CC contraceptives. Finally they can also be used for cell separation in  
 CC vitro by selectively killing unwanted types of cells (e.g. in bone  
 CC marrow) prior to transplantation into a patient undergoing marrow  
 CC ablation by radiation or for killing leukemia cells or T-cells that would  
 CC cause graft-versus-host disease. This sequence represents a bullfrog

CC cytotoxic fusion proteins. They can be used for treatment of cancer and  
 CC autoimmune diseases  
 XX  
 SQ Sequence 110 AA;

Query Match 99.2%; Score 601; DB 2; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 7.9e-61;  
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SNWATFOQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFIISATTVKAICTGVINNVVL 61  
 DB 1 SNWATFOQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFIISATTVKAICTGVINNVVL 60  
 QY 62 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYVHFAGIGRCP 111  
 DB 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYVHFAGIGRCP 110

RESULT 4  
 AAY28872  
 ID AAY28872 standard; protein; 110 AA.

AC AAY28872;  
 XX  
 DT 25-JAN-2000 (first entry)  
 XX  
 DE Rana catesbeiana oocyte ribonuclease (RaCOR1) amino acid sequence.

XX Rana catesbeiana oocyte ribonuclease; RaCOR1; covalently bound; CD22;  
 KW LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's Sarcoma;  
 KW human chorionic gonadotrophin; hCG; recombinant ribonuclease; bullfrog;  
 KW signal peptide; cytotoxic fusion protein; cancer; autoimmune disease;  
 KW RNase.

XX Rana catesbeiana.  
 OS Synthetic.  
 XX  
 XX WO9950398-A2.

XX 07-OCT-1999.  
 XX 26-MAR-1999; 99WO-US006641.  
 XX 27-MAR-1998; 98US-0079751P.  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Rybak SM, Newton DL;  
 XX WPI; 1999-610847/52.  
 XX N-PSDB; AA208130.

XX New recombinant ribonucleases, used for killing target cells, e.g. for  
 PT treating cancers, viral infections or autoimmune diseases.

XX Claim 22; Page 62; 71pp; English.

XX The present sequence is a Rana catesbeiana oocyte ribonuclease (RaCOR1)  
 CC protein encoded by a cDNA modified for expression in E. coli. Carboxy  
 CC terminal end of RaCOR1 has a covalently bound ligand binding moiety,  
 CC which can be a LL2 antibody directed against CD22 on cancerous B cells or  
 CC human chorionic gonadotrophin (hCG) effective against Kaposi's Sarcoma  
 CC cells. Recombinant ribonucleases can be expressed in bacteria without an  
 CC N-terminal methionine due to the presence of a signal peptide that is  
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the  
 CC proteins to be fused in-frame with ligand binding moieties to form  
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and  
 CC autoimmune diseases

XX Sequence 110 AA;

Query Match 98.5%; Score 597; DB 2; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-60;

Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 NWATFOQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFIISATTVKAICTGVINNVVL 62  
 DB 2 NWATFOQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFIISATTVKAICTGVINNVVL 61  
 QY 63 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYVHFAGIGRCP 111  
 DB 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYVHFAGIGRCP 110

RESULT 5  
 AAY28876

ID AAY28876 standard; protein; 111 AA.

AC AAY28876;

XX 25-JAN-2000 (first entry)

XX Recombinant Met(-1) RaCOR1 Met22Leu Met57Leu-(His)6 protein.

XX Met(-1) Rana catesbeiana ribonuclease Met22Leu Met57Leu-(His)6; RaCOR1;  
 KW recombinant; CD22; covalently bound; LL2 antibody; ligand binding moiety;  
 KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;  
 KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;  
 KW cancer; bullfrog; RNase; autoimmune disease.

XX Rana catesbeiana.  
 OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"

FT Misc-difference 1 /note= "(His)6 histidine tag attached to N-terminal Met"

FT Misc-difference 23 /note= "Wild type Met replaced with Leu"

FT Misc-difference 58 /note= "Wild type Met replaced with Leu"

XX WO9950398-A2.

XX 07-OCT-1999.

XX 26-MAR-1999; 99WO-US006641.

XX 27-MAR-1998; 98US-0079751P.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Rybak SM, Newton DL;

XX WPI; 1999-610847/52.

XX N-PSDB; AA208133.

XX New recombinant ribonucleases, used for killing target cells, e.g. for  
 PT treating cancers, viral infections or autoimmune diseases.

XX Claim 22; Page 66; 71pp; English.

XX The present sequence is a recombinant Rana catesbeiana oocyte  
 CC ribonuclease (RaCOR1) protein with Met at position 1 attached to a (His)6  
 CC tag, Met23Leu and Met58Leu. Carboxy terminal end of recombinant RaCOR1  
 CC has a covalently bound ligand binding moiety, which can be a LL2 antibody  
 CC directed against CD22 on cancerous B cells or human chorionic  
 CC gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant  
 CC ribonucleases can be expressed in bacteria without an N-terminal  
 CC methionine due to the presence of a signal peptide that is cleaved by  
 CC bacteria. The soluble expression of ribonuclease allows the proteins to  
 CC be fused in-frame with ligand binding moieties to form cytotoxic fusion  
 CC proteins. They can be used for treatment of cancer and autoimmune  
 CC diseases

XX

CC can be a LL2 antibody directed against CD22 on cancerous B cells or human  
 CC chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.  
 CC Recombinant ribonucleases can be expressed in bacteria without an N-  
 CC terminal methionine due to the presence of a signal peptide that is  
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the  
 CC proteins to be fused in-frame with ligand binding moieties to form  
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and  
 CC autoimmune diseases  
 XX Sequence 111 AA;

Query Match 100.0%; Score 606; DB 2; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-61;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSNWATFQQKHIIPTPIICNTIMDNIIYVGGQCKRVNTFIISATTVKAICTGVINNV 60  
 DB 1 MSNWATFQQKHIIPTPIICNTIMDNIIYVGGQCKRVNTFIISATTVKAICTGVINNV 60  
 QY 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111  
 DB 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111

RESULT 2  
 AAY28873  
 ID AAY28873 standard; protein; 111 AA.

XX AC AAY28873;  
 XX DT 25-JAN-2000 (first entry)  
 XX DE Recombinant Met (-1) RaCOR1.  
 XX KW Recombinant Met (-1) Rana catesbeiana oocyte ribonuclease; RaCOR1; CD22;  
 XX KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;  
 XX KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;  
 XX KW recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;  
 XX KW RNase; autoimmune disease.  
 XX OS Rana catesbeiana.  
 XX OS Synthetic.

XX FH Key Location/Qualifiers  
 XX FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"  
 XX FT

XX PN WO9950398-A2.  
 XX PD 07-OCT-1999.  
 XX PF 26-MAR-1999; 99WO-US006641.  
 XX PR 27-MAR-1998; 98US-0079751P.  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX PI Rybak SM, Newton DL;  
 XX DR WPI; 1999-610847/52.  
 XX DR N-PSDB; AAZ08131.  
 XX FT New recombinant ribonucleases, used for killing target cells, e.g. for  
 XX FT treating cancers, viral infections or autoimmune diseases.  
 XX PS Claim 22; Page 63; 71pp; English.

XX CC The present sequence is a recombinant Rana catesbeiana oocyte  
 CC ribonuclease (RaCOR1) protein with Met at position 1. Carboxy terminal  
 CC end of recombinant RaCOR1 has a covalently bound ligand binding moiety,  
 CC which can be a LL2 antibody directed against CD22 on cancerous B cells or  
 CC human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma  
 CC cells. Recombinant ribonucleases can be expressed in bacteria without an

CC N-terminal methionine due to the presence of a signal peptide that is  
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the  
 CC proteins to be fused in-frame with ligand binding moieties to form  
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and  
 CC autoimmune diseases  
 XX Sequence 111 AA;

Query Match 99.3%; Score 602; DB 2; Length 111;  
 Best Local Similarity 99.1%; Pred. No. 6.1e-61;  
 Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MSNWATFQQKHIIPTPIICNTIMDNIIYVGGQCKRVNTFIISATTVKAICTGVINNV 60  
 DB 1 MQNWATFQQKHIIPTPIICNTIMDNIIYVGGQCKRVNTFIISATTVKAICTGVINNV 60  
 QY 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111  
 DB 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111

RESULT 3  
 AAY28877  
 ID AAY28877 standard; protein; 110 AA.

XX AC AAY28877;  
 XX DT 25-JAN-2000 (first entry)  
 XX DE Recombinant RaCOR1 GlnSer amino acid sequence.

XX KW Recombinant Rana catesbeiana oocyte ribonuclease; RaCOR1 GlnSer; CD22;  
 XX KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;  
 XX KW bullfrog; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; RNase;  
 XX KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;  
 XX KW cancer; autoimmune disease.

XX OS Rana catesbeiana.  
 XX OS Synthetic.

XX FH Key Location/Qualifiers  
 XX FT Misc-difference 1 /note= "Wild type Gln replaced with Ser"  
 XX FT

XX PN WO9950398-A2.  
 XX PD 07-OCT-1999.  
 XX PF 26-MAR-1999; 99WO-US006641.  
 XX PR 27-MAR-1998; 98US-0079751P.  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX PI Rybak SM, Newton DL;  
 XX DR WPI; 1999-610847/52.  
 XX DR N-PSDB; AAZ08131.  
 XX FT New recombinant ribonucleases, used for killing target cells, e.g. for  
 XX FT treating cancers, viral infections or autoimmune diseases.  
 XX PS Claim 22; Page 67; 71pp; English.

XX CC The present sequence is a recombinant Rana catesbeiana oocyte  
 CC ribonuclease (RaCOR1) protein with GlnSer. Carboxy terminal end of  
 CC recombinant RaCOR1 has a covalently bound ligand binding moiety, which  
 CC can be a LL2 antibody directed against CD22 on cancerous B cells or human  
 CC chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.  
 CC Recombinant ribonucleases can be expressed in bacteria without an N-  
 CC terminal methionine due to the presence of a signal peptide that is  
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the  
 CC proteins to be fused in-frame with ligand binding moieties to form

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OM protein - protein search, using sw model  
Run on: May 11, 2004, 14:23:43 ; Search time 50.7285 Seconds  
(without alignments)  
618.248 Million cell updates/sec

Title: US-09-961-400-26  
Perfect score: 606  
Sequence: 1 MSNATFQKHINTPIICN.....ICVKCNQVPVHFAGIGRCP 111

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Jan04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	606	100.0	111	2	AAY28878 Recombina
2	602	99.3	111	2	AAY28873 Recombina
3	601	99.2	110	2	AAY28877 Recombina
4	597	98.5	110	2	AAY28872 Recombina
5	596	98.3	111	2	AAY28876 Recombina
6	591	97.5	110	2	AAY28874 Recombina
7	586.5	96.8	111	2	AAY33321 Frog lect
8	285.5	47.1	105	2	AAY28871 Recombina
9	282.5	46.6	104	2	AAY28871 Recombina
10	281.5	46.5	102	2	AAY28867 Recombina
11	281.5	46.5	112	2	AAY35118 R. pipien
12	281.5	46.5	251	2	AAY35134 R. pipien
13	281.5	46.5	254	2	AAY35135 R. pipien
14	281.5	46.5	355	2	AAY35133 R. pipien
15	281.5	46.5	355	2	AAY35129 R. pipien
16	281.5	46.5	366	2	AAY35132 R. pipien
17	280.5	46.3	104	2	AAY28870 Recombina
18	278.5	46.0	105	2	AAY28869 Recombina
19	277.5	45.8	105	2	AAY35123 R. pipien
20	277.5	45.8	105	2	AAY39400 Recombina
21	277.5	45.8	355	2	AAY35125 R. pipien
22	277.5	45.8	358	2	AAY35130 R. pipien
23	276.5	45.6	104	2	AAY28865 Rana pipi
24	276.5	45.6	105	2	AAY35116 R. pipien
25	276.5	45.6	127	2	AAY28879 Rana pipi

26	273.5	45.1	104	2	AAY28866	Aay28866 Recombina
27	272.5	45.0	104	2	AAR12344	Aar12344 Protein w
28	272.5	45.0	104	2	AAR47303	Aar47303 ONCONASE
29	272.5	45.0	104	2	AAW00736	AAW00736 Protein d
30	272.5	45.0	104	2	AAW14065	AAW14065 Onconase
31	272.5	45.0	104	2	AAW06543	AAW06543 Antitumou
32	272.5	45.0	104	2	AAW30301	AAW30301 Recombina
33	272.5	45.0	104	2	AAW88233	AAW88233 Rana pipi
34	272.5	45.0	104	2	AAY33322	Aay33322 Frog onco
35	272.5	45.0	104	4	AAAB31666	AAAB31666 Amino aci
36	272.5	45.0	104	5	ABG32650	ABG32650 Northern
37	272.5	45.0	107	2	AAW35122	AAW35122 R. pipien
38	272.5	45.0	107	2	AAW35117	AAW35117 R. pipien
39	272.5	45.0	358	2	AAW35127	AAW35127 R. pipien
40	272.5	45.0	365	2	AAW35131	AAW35131 R. pipien
41	272.5	45.0	379	2	AAW35126	AAW35126 R. pipien
42	270.5	44.6	105	2	AAW35115	AAW35115 R. pipien
43	269.5	44.5	104	2	AAW30302	AAW30302 Recombina
44	267.5	44.1	104	4	AAAB31667	AAAB31667 Amino aci
45	267.5	44.1	104	5	ABG31617	ABG31617 Northern

ALIGNMENTS

RESULT 1

AAAY28878	
ID	AAAY28878 standard; protein; 111 AA.
XX	
AC	AAAY28878;
XX	
DT	25-JAN-2000 (first entry)
XX	
DE	Recombinant Met(-1) RaCOR1 Gln1Ser amino acid sequence.
XX	
KW	Recombinant Met(-1) Rana catesbeiana oocyte ribonuclease Gln1Ser; RaCOR1; covalently bound; IL2 antibody; ligand binding moiety; cancerous B cell;
KW	Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;
KW	recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
KW	CD22; RNase; autoimmune disease.
XX	
OS	Rana catesbeiana.
OS	Synthetic.
XX	
FH	Key
FT	Misc-difference 1 /note= "Met not found in wild type RaCOR1"
FT	Misc-difference 2 /note= "Wild type Gln replaced with Ser"
FT	
XX	
XX	WO9950398-A2.
XX	
PD	07-OCT-1999.
XX	
PF	26-MAR-1999; 99WO-US006641.
XX	
PR	27-MAR-1998; 98US-0079751P.
XX	
PA	(USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX	
PI	Rybak SM, Newton DL;
XX	
PI	WPI; 1999-610847/52.
XX	
DR	N-PSDB; AAZ08135.
XX	
DR	New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
XX	
PS	Claim 22; Page 68; 71pp; English.
XX	
CC	The present sequence is a recombinant Rana catesbeiana ribonuclease (RaCOR1) protein with Met at position 1 and Gln2Ser. Carboxy terminal end of recombinant RaCOR1 has a covalently bound ligand binding moiety, which
CC	

Search completed: May 11, 2004, 14:37:53  
Job time : 16.4253 secs

## RESULT 13

US-08-467-955-1  
; Sequence 1, Application US/08467955  
; Patent No. 5728805  
; GENERAL INFORMATION:  
; APPLICANT: Ardelt Ph.D. Wojciech J.  
; TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Mark H. Jay, P.A.  
; STREET: P.O. Box E  
; CITY: Short Hills  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07078-0383  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,955  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/178,118  
; FILING DATE: 06-APR-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/436,141  
; FILING DATE: 13-NOV-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/814,332  
; FILING DATE: 03-FEB-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/283,970  
; FILING DATE: 01-AUG-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jay, Mark H.  
; REGISTRATION NUMBER: 27507  
; REFERENCE/DOCKET NUMBER: 5007 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-912-9066  
; TELEFAX: 201-912-0442  
; TELEX: No. 5728805 Applicable  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 104 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHEICAL: N  
; ANTI-SENSE: N  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: Rana pipiens  
; DEVELOPMENTAL STAGE: Oocyte  
US-08-467-955-1

Query Match 45.3%; Score 272.5; DB 1; Length 104;  
Best Local Similarity 49.1%; Pred. No. 3.5e-24;  
Matches 54; Conservative 15; Mismatches 32; Indels 9; Gaps 4;  
QY 2 NWATFOOKHLINT-PIICNTIMDNIIYVGQCKRVNTFTLISSATTVKAICTGVI-MNMV 59  
DB 2 DMLTFQKKHITNRDVCNDIMSTNLF---HCKDKNTFTYSRPEPVKAIKGLIASKNV 57  
QY 60 LSTTRQLNCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRC 109  
DB 58 LTTSEFVLSDC---NVTSECKYKLLKSKTNKFCVTENQAPVHFVGVGSC 104

## RESULT 14

US-08-891-848-13  
; Sequence 13, Application US/08891848  
; Patent No. 5955073  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Youle, Richard J.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: Nicholls, Peter J.  
; TITLE OF INVENTION: Selective RNase Cytotoxic Reagents  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/891,848  
; FILING DATE: No. 5955073 yet assigned  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/125,462  
; FILING DATE: 22-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/014,082  
; FILING DATE: 04-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/779,195  
; FILING DATE: 22-OCT-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/510,696  
; FILING DATE: 20-APR-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 015280-110310US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 104 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..104  
; OTHER INFORMATION: /label= Onc  
; OTHER INFORMATION: /note= "Onconase from Rana pipiens"  
US-08-891-848-13

Query Match 45.3%; Score 272.5; DB 2; Length 104;  
Best Local Similarity 49.1%; Pred. No. 3.5e-24;  
Matches 54; Conservative 15; Mismatches 32; Indels 9; Gaps 4;  
QY 2 NWATFOOKHLINT-PIICNTIMDNIIYVGQCKRVNTFTLISSATTVKAICTGVI-MNMV 59  
DB 2 DMLTFQKKHITNRDVCNDIMSTNLF---HCKDKNTFTYSRPEPVKAIKGLIASKNV 57  
QY 60 LSTTRQLNCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRC 109  
DB 58 LTTSEFVLSDC---NVTSECKYKLLKSKTNKFCVTENQAPVHFVGVGSC 104

## RESULT 15

Db 319 VLTTFSEFYLSDC---NVTSRPCKYKLIKSTNNKFCVTCENQAPVHFVGVGSC 366

[illegible]

Query Match 45.3%; Score 272.5; DB 1; Length 104;  
Best Local Similarity 49.1%; Pred. No. 3.5e-24;  
Matches 54: Conservative 15; Mismatches 32; Indels 9; Gaps 4

Query Match 45.3%; Score 272.5; DB 1; Length 104;  
Best Local Similarity 49.1%; Pred. No. 3.5e-24;  
Matches 54: Conservative 15; Mismatches 32; Indels 9; Gaps 4





APPLICANT: Wlodawer, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
SEQUENCE CHARACTERISTICS:  
LENGTH: 254 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-875-811-61

Query Match 46.0%; Score 276.5; DB 3; Length 254;  
Best Local Similarity 49.5%; Pred. No. 3.6e-24;  
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;  
Qy 1 SNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFIISATTVKAICTGVI-NMN 58  
Db 2 SDMLTFQKKHITNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57  
Qy 59 VLSTTRFQLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109  
Db 58 VLTTSEFLSDC---NVTSPCKYKLLKSTNKFVTCENQAPVHFVGVGSC 105

RESULT 7  
US-08-875-811-49  
Sequence 49, Application US/08875811  
Patent No. 6045793  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Boque, Lluís  
APPLICANT: Wlodawer, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-875-811-49

Query Match 46.0%; Score 276.5; DB 3; Length 355;  
Best Local Similarity 49.5%; Pred. No. 5.4e-24;  
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;  
Qy 1 SNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFIISATTVKAICTGVI-NMN 58  
Db 252 SDMLTFQKKHITNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 307  
Qy 59 VLSTTRFQLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109  
Db 308 VLTTSEFLSDC---NVTSPCKYKLLKSTNKFVTCENQAPVHFVGVGSC 355

RESULT 8  
US-08-875-811-57  
Sequence 57, Application US/08875811  
Patent No. 6045793  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Boque, Lluís  
APPLICANT: Wlodawer, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,800

DEVELOPMENTAL STAGE: Oocyte  
US-08-467-955-2

Query Match 47.0%; Score 282.5; DB 1; Length 104;

Best Local Similarity 50.0%; Pred. No. 2.4e-25; Mismatches 15; Indels 9; Gaps 4;

QY 2 NWATFOQKHINT-PIICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVI-NMNV 59

Db 2 DWLTFQKHVITRDVDCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIATSKN 57

QY 60 LETTFQQLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109

Db 58 LTTSEFYLSDC---NVTSPCKYKLKSTNKFVTCENQAPVHFVGVGRC 104

## RESULT 4

US-08-875-811-32  
; Sequence 32, Application US/08875811  
; Patent No. 6045793  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: Boque, Lluís  
; APPLICANT: Wlodawer, Alexander  
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811

FILING DATE: 19-FEB-1998

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: WO PCT/US97/02588

FILING DATE: 19-FEB-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/011,800

FILING DATE: 21-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: Paris, Susan K.

REGISTRATION NUMBER: 41,739

REFERENCE/DOCKET NUMBER: 015280-244100US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 112 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-875-811-32

Query Match 46.0%; Score 276.5; DB 3; Length 112;

Best Local Similarity 49.5%; Pred. No. 1.3e-24; Mismatches 15; Indels 9; Gaps 4;

QY 1 SNWATFOQKHINT-PIICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVI-NMN 58

Db 9 SDWLFQKHVITRDVDCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIATSKN 64

QY 59 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109

Db 65 VLTTFSEFYLSDC---NVTSPCKYKLKSTNKFVTCENQAPVHFVGVGSC 112

## RESULT 5

US-08-875-811-59  
; Sequence 59, Application US/08875811  
; Patent No. 6045793  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: Boque, Lluís  
; APPLICANT: Wlodawer, Alexander  
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811

FILING DATE: 19-FEB-1998

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: WO PCT/US97/02588

FILING DATE: 19-FEB-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/011,800

FILING DATE: 21-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: Paris, Susan K.

REGISTRATION NUMBER: 41,739

REFERENCE/DOCKET NUMBER: 015280-244100US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 59:

SEQUENCE CHARACTERISTICS:

LENGTH: 251 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-875-811-59

Query Match 46.0%; Score 276.5; DB 3; Length 251;

Best Local Similarity 49.5%; Pred. No. 3.5e-24; Mismatches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 SNWATFOQKHINT-PIICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVI-NMN 58

Db 148 SDWLFQKHVITRDVDCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIATSKN 203

QY 59 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109

Db 204 VLTTFSEFYLSDC---NVTSPCKYKLKSTNKFVTCENQAPVHFVGVGSC 251

## RESULT 6

US-08-875-811-61  
; Sequence 61, Application US/08875811  
; Patent No. 6045793  
; GENERAL INFORMATION:

APPLICANT: Rybak, Susanna M.

APPLICANT: Newton, Dianne L.

APPLICANT: Boque, Lluís



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 11, 2004, 14:33:03 ; Search time 16.4253 Seconds  
(without alignments)  
345.738 Million cell updates/sec

Title: US-09-961-400-24  
Perfect score: 601  
Sequence: 1 SNWAFQKHIINTPICNT.....ICVKCNQYPVHFAGIGRCP 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	586.5	97.6	111	2	US-08-891-848-12
2	586.5	97.6	111	3	US-08-875-811-8
3	282.5	47.0	104	1	US-08-467-955-2
4	276.5	46.0	112	3	US-08-875-811-32
5	276.5	46.0	251	3	US-08-875-811-59
6	276.5	46.0	254	3	US-08-875-811-61
7	276.5	46.0	355	3	US-08-875-811-49
8	276.5	46.0	355	3	US-08-875-811-57
9	276.5	46.0	355	3	US-08-875-811-64
10	276.5	46.0	366	3	US-08-875-811-55
11	272.5	45.3	104	1	US-08-283-971-1
12	272.5	45.3	104	1	US-07-921-619-1
13	272.5	45.3	104	1	US-08-467-955-1
14	272.5	45.3	104	2	US-08-891-848-13
15	272.5	45.3	104	3	US-08-875-811-1
16	272.5	45.3	104	3	US-09-394-268-1
17	272.5	45.3	104	4	US-09-071-672-1
18	272.5	45.3	104	4	US-09-687-748-1
19	272.5	45.3	104	4	US-08-626-288-1
20	272.5	45.3	104	4	US-09-095-429-1
21	272.5	45.3	104	4	US-09-986-119-1
22	272.5	45.3	105	3	US-08-875-811-39
23	272.5	45.3	106	3	US-08-875-811-28
24	272.5	45.3	107	3	US-08-875-811-30
25	272.5	45.3	129	3	US-08-875-811-63
26	272.5	45.3	353	3	US-08-875-811-41
27	272.5	45.3	358	3	US-08-875-811-51

28	272.5	45.3	379	3	US-08-875-811-43	Sequence 43, Appl
29	271.5	45.2	105	3	US-08-875-811-26	Sequence 26, Appl
30	269.5	44.8	104	4	US-08-626-288-2	Sequence 2, Appl
31	269.5	44.8	104	4	US-09-095-429-2	Sequence 2, Appl
32	267.5	44.5	104	3	US-09-394-268-2	Sequence 2, Appl
33	267.5	44.5	104	4	US-09-687-748-2	Sequence 2, Appl
34	267.5	44.5	105	3	US-08-875-811-24	Sequence 24, Appl
35	267.5	44.5	358	3	US-08-875-811-45	Sequence 45, Appl
36	267.5	44.5	365	3	US-08-875-811-53	Sequence 53, Appl
37	253.5	42.2	107	3	US-08-875-811-20	Sequence 20, Appl
38	239.5	39.9	111	3	US-08-875-811-22	Sequence 22, Appl
39	235	39.1	114	3	US-09-223-118-3	Sequence 3, Appl
40	231.5	38.5	360	3	US-08-875-811-47	Sequence 47, Appl
41	226	37.6	114	3	US-09-223-118-2	Sequence 2, Appl
42	225	37.4	114	3	US-09-223-118-1	Sequence 1, Appl
43	224	37.3	114	3	US-09-223-118-4	Sequence 4, Appl
44	206	34.3	83	3	US-08-875-811-2	Sequence 2, Appl
45	206	34.3	83	4	US-09-071-672-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1  
US-08-891-848-12  
; Sequence 12, Application US/08891848  
; Patent No. 5955073  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Youle, Richard J.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: Nicholls, Peter J.  
; TITLE OF INVENTION: Selective RNase Cytotoxic Reagents  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/891,848  
; FILING DATE: No. 5955073 yet assigned  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/125,462  
; FILING DATE: 22-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/014,082  
; FILING DATE: 04-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/779,195  
; FILING DATE: 22-OCT-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/510,696  
; FILING DATE: 20-APR-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 015280-110310US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 111 amino acids  
; TYPE: amino acid

Search completed: May 11, 2004, 14:35:04  
Job time : 9.95475 secs



[illegible]









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RT RT fibroblasts.
RL Mol. Cell. Biol. 17:1503-1512(1997).
CC -!- FUNCTION: Angiogenin induces vascularization of normal and
CC malignant tissues. Abolishes protein synthesis by specifically
CC hydrolyzing cellular tRNAs (By similarity).
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL: U72672; AAC05794.1; -.
CC HSP: P10152; IAGI.
CC MGD: MGI:1201793; Angl.
CC InterPro: IPR001427; RNaseA.
CC Pfam: PF00074; rnaseA; 1.
CC PRINTS: PR00794; RNaseA; 1.
CC ProDom: PD000535; RNaseA; 1.
CC SMART: SM00092; RNase Pc; 1.
CC PROSITE: PS00127; RNASE_PANCREATIC; 1.
CC Signal: Hydrolase; Nuclease; Pyrolidone carboxylic acid.
CC KW Pyrolidone carboxylic acid.
CC FT SIGNAL 1 24
CC FT CHAIN 25 145
CC FT MOD_RES 25 25
CC FT ACT_SITE 37 37
CC FT ACT_SITE 64 64
CC FT ACT_SITE 137 137
CC FT ACT_SITE 104 104
CC FT DISULFID 50 104
CC FT DISULFID 63 115
CC FT DISULFID 81 130
CC SQ SEQUENCE 145 AA; 16696 MW; D89D3BC92FD1D682C CRC64;
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CC Query Match 25.7%; Score 154.5; DB 1; Length 145;
CC Best Local Similarity 43.6%; Pred. No. 1e-09;
CC Matches 34; Conservative 12; Mismatches 23; Indels 9; Gaps 4;
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CC QY 33 CKRVNTFIISATTVKAIC-----TGVNNVNLSTTRFQNTCTRTSITPR-PCPYSSR 85
CC ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
CC 63 CKVNTFIHDTKNNKAICGNGRPGYGV-NPRI-SNSRFQVTTCTHKGSPPPCQYNAF 120
CC ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
CC
CC QY 86 TETNYICVKCNQYVHF 103
CC : ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
CC 121 KQRYIVACEDGMPVHF 138
CC
CC RESULT 6
CC ANGR MOUSE
CC ID -ANGR MOUSE STANDARD; PRT; 145 AA.
CC AC Q64438;
CC DT 01-NOV-1997 (Rel. 35, Created)
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Angiogenin-related protein precursor.
CC ANGRP.
CC OS Mus musculus (Mouse).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC NCBI_TaxID=10090;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=129; TISSUE=Liver;
CC RX MEDLINE=86079109; PubMed=8530072;
CC RA Brown W.E., Nobile V., Subramanian V., Shapiro R.;
CC RT "The mouse angiogenin gene family: structures of an angiogenin-related
CC RT protein gene and two pseudogenes.";
CC RL Genomics 29:200-206(1995).
CC
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL: U23519; AAA91367.1; -.
CC HSP: P03950; I44Y.
CC MGD: MGI:104984; Angrip.
CC InterPro: IPR001427; RNaseA.
CC Pfam: PF00074; rnaseA; 1.
CC PRINTS: PR00794; RNaseA; 1.
CC ProDom: PD000535; RNaseA; 1.
CC SMART: SM00092; RNase Pc; 1.
CC PROSITE: PS00127; RNASE_PANCREATIC; 1.
CC Signal: Hydrolase; Nuclease; Pyrolidone carboxylic acid.
CC KW Pyrolidone carboxylic acid.
CC FT SIGNAL 1 24
CC FT CHAIN 25 145
CC FT MOD_RES 25 25
CC FT ACT_SITE 37 37
CC FT ACT_SITE 64 64
CC FT ACT_SITE 137 137
CC FT ACT_SITE 104 104
CC FT DISULFID 50 104
CC FT DISULFID 63 115
CC FT DISULFID 81 130
CC SQ SEQUENCE 145 AA; 16612 MW; 29A6EB814429C4AD CRC64;
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CC Query Match 24.9%; Score 149.5; DB 1; Length 145;
CC Best Local Similarity 43.4%; Pred. No. 3.5e-09;
CC Matches 33; Conservative 10; Mismatches 28; Indels 5; Gaps 3;
CC
CC QY 33 CKRVNTFIISATTVKAIC--TGVNNV-LSTTRFQNTCTRTSITPR-PCPYSSRTE 87
CC ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
CC 63 CKDVTFIHDTKNNKAICGKSGPYGRNLRISKRFQVTTCTHKGSPPPCPYRASKG 122
CC ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
CC
CC QY 88 TNYICVKCNQYVHF 103
CC ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
CC 123 FRYIIIGCENGMPVHF 138
CC
CC RESULT 7
CC RNP_BALAC
CC ID -RNP_BALAC STANDARD; PRT; 124 AA.
CC AC P00673;
CC DT 21-JUL-1986 (Rel. 01, Created)
CC DT 21-JUL-1986 (Rel. 01, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
CC GN RNASE1 OR RNS1.
CC OS Balaenoptera acutorostrata (Minke whale) (lesser rorqual).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
CC OC Balaenopteridae; Balaenoptera.
CC NCBI_TaxID=9767;
CC RN [1]
CC RP SEQUENCE.
CC RX MEDLINE=76277855; PubMed=962870;
CC RA Emmens M., Welling G.W., Beintema J.J.;
CC RT "The amino acid sequence of pike-whale (lesser-rorqual) pancreatic
CC RT ribonuclease.";
CC RL Biochem. J. 157:317-323(1976).
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Pancreas.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.

```



```

CC residues with a 3'flanking guanine. Hydrolyzes poly(U) and poly(C)
CC as substrates, and prefers the former. The S-lectins in frog eggs
CC may be involved in the fertilization and development of the frog
CC embryo. This lectin agglutinates various animal cells, including
CC normal lymphocytes, erythrocytes, and fibroblasts of animal and
CC human origin. It is cytotoxic against several tumor cells.
CC
CC -!- SUBUNIT: Monomer.
CC
CC -!- SEQUENCE, AND DISULFIDE BONDS.
CC
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AF039104; AAD10702.1; -.
CC PIR; A27121; A27121.
CC PDB; 1BC4; 28-OCT-98.
CC PDB; 1M07; 21-JAN-03.
CC InterPro; IPR001427; RNaseA.
CC Pfam; PF00074; RNaseA; 1.
CC ProDom; PD000535; RNaseA; 1.
CC SMART; SM00092; RNaseA; 1.
CC PROSITE; PS00127; RNASE_PANCREATIC; 1.
CC KW Hydroxylase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure;
CC KW signal; Pyrrolidone carboxylic acid.
CC FT SIGNAL 1 22
CC FT CHAIN 23 133 RIBONUCLEASE, OOCYTES.
CC FT MOD_RES 23 133 PYRROLIDONE CARBOXYLIC ACID.
CC FT ACT_SITE 32 32
CC FT ACT_SITE 57 57
CC FT ACT_SITE 125 125
CC FT DISULFID 41 93
CC FT DISULFID 56 103
CC FT DISULFID 74 118
CC FT DISULFID 115 132
CC FT HELIX 25 32
CC FT HELIX 41 45
CC FT TURN 48 49
CC FT STRAND 59 63
CC FT HELIX 67 73
CC FT TURN 74 74
CC FT STRAND 79 84
CC FT STRAND 90 95
CC FT STRAND 105 110
CC FT STRAND 114 119
CC FT TURN 120 121
CC FT STRAND 122 129
CC SQ SEQUENCE 133 AA; 14762 MW; A7D62594F7D16F0C CRC64;

Query Match 97.6%; Score 586.5; DB 1; Length 133;
Best Local Similarity 99.1%; Pred. No. 3.1e-56;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 NWATFQOKHIINTP-II-CNTIMDNNIYVGQCKRVNTFISSATTVKAICTGVINNNVL 60
DB 24 NWATFQOKHIINTP-II-CNTIMDNNIYVGQCKRVNTFISSATTVKAICTGVINNNVL 83
QY 61 STTRFQOLNCTRTSITPRPCPYSSRTETNYICVKCNQYVPHFAGIGRCP 110
DB 84 STTRFQOLNCTRTSITPRPCPYSSRTETNYICVKCNQYVPHFAGIGRCP 133

RESULT 2
LECS-RANJA STANDARD; PRT; 111 AA.
AC P18839;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

```

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DE DE Sialic acid-binding lectin (EC 3.1.1.27.-).
OS Rana japonica (Japanese redbellied frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
OX NCBI_TaxID=8402;
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RC TISSUE=Egg;
RX MEDLINE=91035319; PubMed=2229005;
RA Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H.,
RA Takayanagi Y., Titani K.;
RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
RT eggs.";
RL J. Biochem. 108:139-143(1990).
CC -!- FUNCTION: The S-lectins in frog eggs may be involved in the
CC fertilization and development of the frog embryo. This lectin
CC preferentially agglutinates a large variety of tumor cells, but it
CC does not agglutinate non-transformed cells and erythrocytes.
CC -!- SUBUNIT: Monomer.
CC
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC
CC PIR; JX0120; JX0120.
DR HSSP; P11316; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR KW Hydroxylase; Nuclease; Endonuclease; Sialic acid; Lectin;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 10 10 BY SIMILARITY.
FT ACT_SITE 35 35 BY SIMILARITY.
FT ACT_SITE 104 104 BY SIMILARITY.
FT DISULFID 19 72
FT DISULFID 34 82
FT DISULFID 52 97
FT DISULFID 94 111
SQ SEQUENCE 111 AA; 12326 MW; FDEBDDF3834ED679 CRC64;

Query Match 74.9%; Score 450; DB 1; Length 111;
Best Local Similarity 78.2%; Pred. No. 1.2e-41;
Matches 86; Conservative 7; Mismatches 15; Indels 2; Gaps 2;

QY 2 NWATFQOKHIINTP-II-CNTIMDNNIYVGQCKRVNTFISSATTVKAICTGV-INNNV 59
DB 2 NWATFQOKHIINTP-II-CNTIMDNNIYVGQCKRVNTFISSATTVKAICTGV-INNNV 61
QY 60 LSTTRFQOLNCTRTSITPRPCPYSSRTETNYICVKCNQYVPHFAGIGRCP 109
DB 62 LSTTRFQOLNCTRTSITPRPCPYSSRTETNYICVKCNQYVPHFAGIGRCP 111

RESULT 3
RNPL-RANCA STANDARD; PRT; 111 AA.
AC P14626;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease, liver (EC 3.1.1.27.5).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=90130374; PubMed=2613682;
RA Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
RA Okazaki T., Ohgi K., Irie M.;
RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
RT liver.";

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 11, 2004, 14:24:28 ; Search time 9.95475 Seconds

(without alignments)  
575.375 Million cell updates/sec

Title: US-09-961-400-24

Perfect score: 601

Sequence: 1 SNWATFQKHINPIICNT.....ICVKCNQYPVHFAGIGRCP 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	586.5	97.6	133	1 RNPO_RANCA	P11916 rana catesb
2	450	74.9	111	1 LECS_RANJA	P18839 rana japoni
3	369	61.4	111	1 RN30_RANCA	P14626 rana catesb
4	272.5	45.3	104	1 RN30_RANPI	P22069 rana pipien
5	154.5	25.7	145	1 ANG_MOUSE	P97802 mus musculu
6	149.5	24.9	145	1 ANGR_MOUSE	Q64438 mus musculu
7	135.5	22.5	124	1 RNP_BALAC	P00673 balaenopter
8	135.5	22.5	145	1 ANGI_MOUSE	P21570 mus musculu
9	133.5	22.2	167	1 RNBR_BOVIN	P39873 bos taurus
10	132.5	22.0	124	1 RNP_PIG	P00671 sus scrofa
11	128.5	21.4	151	1 RNBR_CAPCA	P79351 capreolus c
12	127.5	21.2	123	1 ANG2_BOVIN	P80929 bos taurus
13	127.5	21.2	141	1 RNBR_GIRCA	Q29542 giraffa cam
14	127.5	21.2	151	1 RNBR_AXIPR	P87350 axis porcin
15	126.5	21.0	119	1 RNP_IGUIT	P80287 iguana igua
16	126.5	21.0	146	1 ANGI_CEEAE	Q8wn66 cercopithec
17	126.5	21.0	146	1 ANGI_MOTA	Q8wn65 miopithecus
18	125	20.8	143	1 ANGI_SAISC	Q8wn60 saimiri sci
19	123.5	20.5	143	1 RNBR_SHEEP	Q29543 ovis aries
20	122.5	20.4	124	1 RNP_ANTAM	P00668 antilocapra
21	122	20.3	122	1 RNP_MACRU	P00686 macropus ru
22	120.5	20.0	128	1 RNP_MYOCO	P00676 myocastor c
23	120.5	20.0	147	1 ANGI_PONPY	Q8wn67 pongo pygma
24	120.5	20.0	149	1 RNP_MOUSE	P00683 mus musculu
25	120	20.0	146	1 ANGI_AOTTR	Q8wn61 aotus trivi
26	119.5	19.9	123	1 ANGI_PIG	P31346 sus scrofa
27	118.5	19.7	128	1 RNBP_CAVPO	P00679 saguinus oe
28	117.5	19.6	146	1 ANGI_SAGOE	Q8wn62 saguinus oe
29	117.5	19.6	128	1 RNP_HORSE	P00674 equus caball
30	116.5	19.4	124	1 RNP_CAMDR	P00670 camelus dro
31	116.5	19.4	128	1 RNP_PROGU	P04059 proechinys
32	115.5	19.2	119	1 RNS4_BOVIN	P15467 bos taurus
33	115.5	19.2	146	1 ANGI_MACMU	Q8wn63 macaca mula

RESULT 1  
RNPO\_RANCA STANDARD; PRT; 133 AA.  
ID RNPO\_RANCA  
AC P11916; Q9PWR7;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ribonuclease, oocytes precursor (EC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SBL-C).  
GN RCR.  
OS Rana catesbeiana (Bull frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
ON NCBI\_TaxID=8400;  
RX MEDLINE=87299649; PubMed=3304421;  
TX Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;  
RT "The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.  
RT Tissue distribution, cloning, purification, cytotoxicity, and active  
RT residues for RNase activity";  
RL J. Biol. Chem. 273:6395-6401(1998).  
[2]  
RN SEQUENCE OF 23-133.  
TISSUE=Egg;  
RX MEDLINE=87299649; PubMed=3304421;  
TX Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,  
Takayanagi G., Hakomori S.;  
RA "Amino acid sequence of sialic acid binding lectin from frog (Rana  
R catesbeiana) eggs.";  
RL Biochemistry 26:2189-2194(1987).  
[3]  
RN CHARACTERIZATION, AND SEQUENCE OF 81-101.  
RX MEDLINE=92220613; PubMed=1373237;  
TX Liao Y.-D.;  
RA "A pyrimidine-guanine sequence-specific ribonuclease from Rana  
R catesbeiana (bullfrog) oocytes.";  
RL Nucleic Acids Res. 20:1371-1377(1992).  
[4]  
RN CHARACTERIZATION.  
TISSUE=Egg;  
RX MEDLINE=93192604; PubMed=8448385;  
TX Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,  
Takayanagi Y., Hakomori S., Titani K.;  
RA "Ribonuclease activity of sialic acid-binding lectin from Rana  
R catesbeiana eggs.";  
RL Glycobiology 3:37-45(1993).  
[5]  
RN STRUCTURE BY NMR OF 23-133.  
RX MEDLINE=98437383; PubMed=9761686;  
TX Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;  
RA "The solution structure of a cytotoxic ribonuclease from the oocytes  
RT of Rana catesbeiana (bullfrog).";  
RL J. Mol. Biol. 283:231-244(1998).  
CC -!- FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine

## ALIGNMENTS

34 114 19.0 148 1 ANGI\_BOVIN P10152 bos taurus  
35 113.5 18.9 124 1 RNP\_RANTA P00666 rangifer ta  
36 113.5 18.9 125 1 ANGI\_RABIT P31347 oryctolagus  
37 113.5 18.9 146 1 ANGI\_PAPHA Q8wn64 papio hamad  
38 113 18.8 147 1 ANGI\_HUMAN P03950 homo sapien  
39 113 18.8 147 1 ANGI\_PANTR Q8wn68 pan troglod  
40 112.5 18.7 124 1 RNP\_CAPCA P00664 capreolus c  
41 112.5 18.7 124 1 RNP\_GIRCA P00662 giraffa cam  
42 112.5 18.7 148 1 RNS4\_MOUSE Q9jjh1 mus musculu  
43 111.5 18.6 130 1 RNP\_CRILO P24717 cricetus  
44 111.5 18.6 147 1 RNS4\_RAT O55004 rattus norv  
45 111.5 18.6 149 1 RNP\_ACOCA Q9wt55 acomys cahi









```
J. Mol. Evol. 13, 305-316, 1979
A>Title: Primary structure of pronghorn pancreatic ribonuclease: close relationship bet
A:Reference number: A00813; MUID:R0075014; PMID:513141
A:Accession: A00813
A:Molecule type: protein
A:Superfamily: pancreatic ribonuclease
C:Residues: 1-124 <BEI>
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12_41,119/Active site: His, Lys, His #status predicted
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F:34/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
Query Match      20.4%; Score 122.5; DB 1; Length 124;
Best Local Similarity 30.3%; Pred. No. 3.e-05;
Matches 36; Conservative Indels 23; Gaps 7;
QY      4 ATFOQRHINTPI-----ICNTIMDNNIIVGGCKRVNTHFISSATTVCATCTGVNM 57
```

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QY 2 NWATFOQKHINTP-IIICNTIMDNIIYVGGQCKRVNTFISSATTVAICTGV-INNV 59
DB 2 NWAKFQKHINTSINCNTIMDKSIYVGGQCKERNFTFISSATTVAICTGASTNRV 61
QY 60 LSTTRFQNTCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRC 109
DB 62 LSTTRFQNTCTRTSITPRPCPSYSSRTETNYICVKCENRLPVHFAGIGRC 111

RESULT 3
JK0085
C:Species: Rana catesbeiana (bullfrog)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
C:Accession: JX0085
R:Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Ohguchi, J. Biochem. 106, 729-735, 1989
A:Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
A:Reference number: JX0085; MUID:90130374; PMID:2613682
A:Accession: JX0085
A:Molecule type: protein
A:Residues: 1-111 <NIT>
C:Superfamily: pancreatic ribonuclease
C:Keywords: hydrolase; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10,35,104/Active site: His, Lys, His #status predicted
F:19,72,34-82,52-97,94-111/Disulfide bonds: #status predicted

Query Match 61.4%; Score 369; DB 2; Length 111;
Best Local Similarity 65.5%; Pred. No. 9,6e-30;
Matches 72; Conservative 9; Mismatches 27; Indels 2; Gaps 2;

QY 2 NWATFOQKHINTP-IIICNTIMDNIIYVGGQCKRVNTFISSATTVAICTGV-INNV 59
DB 2 NWAKFQKHINTSINCNTIMDKSIYVGGQCKERNFTFISSATTVAICTGASTNRV 61
QY 60 LSTTRFQNTCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRC 109
DB 62 LSTTRFQNTCTRTSITPRPCPSYSSRTETNYICVKCENRLPVHFAGIGRC 111

RESULT 4
A39035
Ribonuclease-related anti-tumor protein - northern leopard frog (fragment)
C:Species: Rana pipiens (northern leopard frog)
C:Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
C:Accession: A39035
R:Ardelet, W.; Mikulski, S.M.; Shogen, K.
J. Biol. Chem. 266, 245-251, 1991
A:Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and early embryos.
A:Reference number: A39035; MUID:91093131; PMID:1985896
A:Accession: A39035
A:Molecule type: protein
A:Residues: 1-104 <ARD>
C:Superfamily: pancreatic ribonuclease

Query Match 45.3%; Score 272.5; DB 2; Length 104;
Best Local Similarity 49.1%; Pred. No. 3.5e-20;
Matches 54; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 2 NWATFOQKHINTP-IIICNTIMDNIIYVGGQCKRVNTFISSATTVAICTGV-INNV 59
DB 2 DWLTFQKHINTDVRDVCNMTNLF----HCKDKNTFIYSRPEPVKAICKGLIASKNV 57
QY 60 LSTTRFQNTCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRC 109
DB 58 LTTSEFYLSDC---NVTSRCPCKYKLNKTSNFKVCVTENQAPVHFVGVGSC 104

RESULT 5
NRWHK
pancreatic ribonuclease (EC 3.1.27.5) - minke whale

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N:Alternate names: RNase 1; RNase A
C:Species: Balaeoptera acutorostrata (minke whale, lesser rorqual)
C:Date: 24-Apr-1994 #sequence_revision 24-Apr-1994 #text_change 03-Jun-1994
C:Accession: A00818
R:Emmens, M.; Welling, G.W.; Beintema, J.J.
Biochem. J. 157, 317-323, 1976
A:Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease.
A:Reference number: A00818; MUID:76277855; PMID:962870
A:Accession: A00818
A:Molecule type: protein
A:Residues: 1-124 <EMM>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12,41,119/Active site: His, Lys, His #status predicted
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F:76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 22.5%; Score 135.5; DB 1; Length 124;
Best Local Similarity 33.3%; Pred. No. 1.7e-06;
Matches 39; Conservative 16; Mismatches 39; Indels 23; Gaps 7;

QY 6 FQOKHII-----NTPICNTIMDNIIYVGGQCKRVNTFISSATTVAICTGVINNV 59
DB 8 FQOKHII-----NTPICNTIMDNIIYVGGQCKRVNTFISSATTVAICTGVINNV 59
QY 60 L-----STTRFQNTCTRTSITPRP-CPYSSRTETNYICVKE-NOY-PVHF 103
DB 64 LCKNGRINCYESNSTMTIDCRQTGSSKYPNCATKTSQKXHIIVACGNYPVHF 120

RESULT 6
A35932
angiogenin precursor - mouse
N:Alternate names: angiogenesis factor
N:Contains: ribonuclease (EC 3.1.27.-)
C:Species: Mus musculus (house mouse)
C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999
C:Accession: A35932
R:Bond, M.D.; Vallee, B.L.
Biochem. Biophys. Res. Commun. 171, 988-995, 1990
A:Title: Isolation and sequencing of mouse angiogenin DNA.
A:Reference number: A35932; MUID:91025023; PMID:2222458
A:Accession: A35932
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-145 <BON>
A:Cross-references: GB:U2516; NID:g726325; PIDN:AAA91366.1; PID:g726326
C:Genetics:
A:Introns: #status absent
C:Function:
A:Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
C:Superfamily: pancreatic ribonuclease
C:Keywords: angiogenesis; hydrolase; nucleic acid degradation; pyroglutamic acid
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-145/Product: angiogenin #status predicted <MAT>
F:25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F:37,64,137/Active site: His, Lys, His #status predicted
F:50-104,63-115,81-130/Disulfide bonds: #status predicted

Query Match 22.5%; Score 135.5; DB 1; Length 145;
Best Local Similarity 39.5%; Pred. No. 2e-06;
Matches 30; Conservative 12; Mismatches 29; Indels 5; Gaps 3;

QY 33 CKRVNTFISSATTVAICTGVINNV-LSTTRFQNTCTRTSITPR-PCPYSSRTE 87
DB 63 CKRVNTFIHGKNIRKAIKANGSPYRENLKMSPPQVTTCXKGTGSPPCQYRASAG 122
QY 88 TNYICVKCENQYPVHF 103
DB 123 FRHVTACENGLPVHF 138

RESULT 7

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 11, 2004, 14:31:13 ; Search time 13.4389 Seconds  
(without alignments)  
787.345 Million cell updates/sec

Title: US-09-961-400-24  
Perfect score: 601  
Sequence: 1 SNWATFOQKHINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78: \*  
1: PIR1: \*  
2: PIR2: \*  
3: PIR3: \*  
4: PIR4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	586.5	97.6	111	2 A27121	ribonuclease-relat
2	450	74.9	111	1 JX0120	ribonuclease-relat
3	369	61.4	111	2 JX0085	pancreatic ribonuc
4	272.5	45.3	104	2 A39035	ribonuclease-relat
5	135.5	22.5	124	1 NRWHK	pancreatic ribonuc
6	135.5	22.5	145	1 A35932	angiogenin precurs
7	133.5	22.2	167	2 S20066	pancreatic-type ri
8	132.5	22.0	124	1 NRPG	pancreatic ribonuc
9	126.5	21.0	119	2 S41111	pancreatic ribonuc
10	122.5	20.4	124	1 NRPRH	pancreatic ribonuc
11	122	20.3	122	1 NRKGR	pancreatic ribonuc
12	120.5	20.0	128	1 NRUCU	pancreatic ribonuc
13	120.5	20.0	149	1 NRMS	pancreatic ribonuc
14	119.5	19.9	123	1 A43825	angiogenin - p19
15	118.5	19.7	128	1 NRGPB	pancreatic ribonuc
16	117.5	19.6	128	1 NRHQ	pancreatic ribonuc
17	116.5	19.4	124	1 NRKM	pancreatic ribonuc
18	116.5	19.4	124	1 NRKM	pancreatic ribonuc
19	116.5	19.4	124	1 NRKM	pancreatic ribonuc
20	116.5	19.4	128	1 NRKS	pancreatic ribonuc
21	114.5	19.1	124	2 S08549	angiogenin - dom
22	114	19.0	125	1 A32474	angiogenin [valida
23	113.5	18.9	124	1 NRDEN	pancreatic ribonuc
24	113.5	18.9	125	1 B43825	angiogenin - rabbi
25	113	18.8	147	1 NRHUG	angiogenin precurs
26	112.5	18.7	124	1 NRGF	pancreatic ribonuc
27	112.5	18.7	124	1 NRDEO	pancreatic ribonuc
28	111.5	18.6	130	2 S22808	pancreatic ribonuc
29	110.5	18.4	124	1 NRBOB	pancreatic ribonuc

30	110.5	18.4	124	1 NRWB	pancreatic ribonuc
31	110.5	18.4	124	1 NREKN	pancreatic ribonuc
32	110.5	18.4	124	2 S07141	pancreatic ribonuc
33	110.5	18.4	150	1 NRBO	pancreatic ribonuc
34	110.5	18.4	158	2 161900	eosinophil-derived
35	109.5	18.2	124	1 NRSH	pancreatic ribonuc
36	108.5	18.1	119	2 JX0115	pancreatic ribonuc
37	108.5	18.1	124	1 NRCH	pancreatic ribonuc
38	108.5	18.1	152	1 NRRT	pancreatic ribonuc
39	106.5	17.7	124	1 NRHP	seminal ribonuclea
40	106.5	17.7	125	4 A47498	seminal ribonuclea
41	106.5	17.7	150	1 NREOS	pancreatic ribonuc
42	104.5	17.4	124	1 NRGN	pancreatic ribonuc
43	104.5	17.4	124	1 NRDEF	pancreatic ribonuc
44	104	17.3	125	2 S04503	pancreatic ribonuc
45	103.5	17.2	124	2 S08546	pancreatic ribonuc

ALIGNMENTS

RESULT 1

A27121  
ribonuclease-related sialic acid-binding lectin - bullfrog  
C;Species: Rana catesbeiana (bullfrog)  
C;Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 30-Jun-1993  
C;Accession: A27121  
R;Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawachi, H.; Takayanagi  
Biochemistry 26, 2189-2194, 1987  
A;Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)  
A;Reference number: A27121; MUID:87299649; PMID:3304421  
A;Accession: A27121  
A;Molecule type: protein  
A;Residues: 1-111 <PI>  
C;Superfamily: pancreatic ribonuclease  
C;Keywords: lectin

Query Match 97.6%; Score 586.5; DB 2; Length 111;  
Best Local Similarity 99.1%; Pred. No. 2.3e-51;  
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
Qy 2 NWATFOQKHINTPII-CNTIMDNIIYVGQCKRVNTFIISATTVKAICTGVINNVL 60  
Db 2 NWATFOQKHINTPIINCNTIMDNIIYVGQCKRVNTFIISATTVKAICTGVINNVL 61  
Qy 61 STTRFQNTCTRTSITPRCPYSRSTETNYICVKCENQYPVHFAGIGRCP 110  
Db 62 STTRFQNTCTRTSITPRCPYSRSTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 2

JX0120  
ribonuclease-related sialic acid-binding lectin - Japanese frog  
C;Species: Rana japonica (Japanese frog)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C;Accession: JX0120  
R;Kamiya, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawachi, H.; Takayanagi  
J. Biochem. 108, 139-143, 1990  
A;Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.  
A;Reference number: JX0120; MUID:91035319; PMID:2229005  
A;Accession: JX0120  
A;Molecule type: protein  
A;Residues: 1-111 <KAM>  
A;Experimental source: egg  
C;Superfamily: pancreatic ribonuclease  
C;Keywords: lectin; pyroglyutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;19-72,34-82,52-97,94-111/Disulfide bonds: #status experimental

Query Match 74.9%; Score 450; DB 1; Length 111;  
Best Local Similarity 78.2%; Pred. No. 8.6e-38;  
Matches 86; Conservative 7; Mismatches 15; Indels 2; Gaps 2;

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XX PD 07-OCT-1999.
XX PF 26-MAR-1999; 99WO-US006641.
XX PR 27-MAR-1998; 98US-0079751P.
XX FA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Rybak SM, Newton DL;
XX PS Disclosure; Page 69; 71pp; English.
XX CC The present sequence is a Rana pipiens Clone Sa1b ribonuclease (RaPLR1).
XX CC It is encoded by Clone Sa1b cDNA obtained from Rana pipiens liver mRNA
XX CC library. It exhibits differences with Onconase (RTM) at amino acid
XX CC residues 11, 20, 85 and 103. Carboxy terminal end of RaPLR1 has a
XX CC covalently bound ligand binding moiety, which can be a L22 antibody
XX CC directed against CD22 on cancerous B cells or human chorionic
XX CC gonadotropin (hCG) effective against Kaposi's Sarcoma cells. Recombinant
XX CC ribonucleases can be expressed in bacteria without an N-terminal
XX CC methionine due to the presence of a signal peptide that is cleaved by
XX CC bacteria. The soluble expression of ribonuclease allows the proteins to
XX CC be fused in-frame with ligand binding moieties to form cytotoxic fusion
XX CC proteins. They can be used for treatment of cancer and autoimmune
XX CC diseases
XX SQ Sequence 127 AA;

Query Match 46.0%; Score 276.5; DB 2; Length 127;
Best Local Similarity 49.1%; Pred. No. 1.4e-23;
Matches 54; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

Qy 2 NWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFIISATTVKAICTGVI-NMN 59
Db 25 DMLTFQKKHLNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 80

Qy 60 LSTTRFQNLNCTRTSITPRCPYSSRTETNYICVKCNQYVPHFAGIGRC 109
Db 81 LTTSEFYLSDC---NVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 15
AAW35134
ID AAW35134 standard; protein; 251 AA.
XX AC AAW35134;
XX DT 20-APR-1998 (first entry)
XX DE R. pipiens recombinant RNase rOnc fusion protein 10.
XX KW RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
XX KW tumour cell growth; frog.
XX OS Rana pipiens.
XX OS Synthetic.
XX PN W09731116-A2.
XX PD 28-AUG-1997.
XX PF 19-FEB-1997; 97WO-US002588.
XX PR 21-FEB-1996; 96US-0011800P.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

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XX PI Rybak SM, Newton DL, Boque L, Wlodawer A;
XX DR WPI; 1997-435168/40.
XX DR N-PSDB; AAT94972.
XX PT Ribonuclease molecules based on native Onconase - used for killing cells,
XX PT particularly tumour cells.
XX PS Disclosure; Page 76; 90pp; English.
XX CC Sequences AAW35125 to AAW35135 represent recombinant fusion proteins
XX CC (rOnc) which are modifications of the RNase Onconase (RTM) (nOnc). Such
XX CC novel ribonuclease molecules are highly cytotoxic and can be used alone
XX CC or to form chemical conjugates or to target recombinant immunofusions.
XX CC They are used particularly for decreasing tumour cell growth. They can
XX CC also be used for cell separation in vitro by selectively killing unwanted
XX CC types of cells, e.g. in bone marrow prior to transplantation into a
XX CC patient undergoing marrow ablation by radiation, or for killing leukaemia
XX CC cells or T-cells that would cause graft versus host disease. The toxins
XX CC can also be used to selectively kill unwanted cells in culture. The new
XX CC ribonucleases have increased cytotoxic activity compared to nOnc and also
XX CC lower immunogenicity in humans
XX SQ Sequence 251 AA;

Query Match 46.0%; Score 276.5; DB 2; Length 251;
Best Local Similarity 49.5%; Pred. No. 3.3e-23;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

Qy 1 SNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFIISATTVKAICTGVI-NMN 58
Db 148 SDMLTFQKKHLNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 203

Qy 59 VLSTTRFQNLNCTRTSITPRCPYSSRTETNYICVKCNQYVPHFAGIGRC 109
Db 204 VLTTSSEFYLSDC---NVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 251

Search completed: May 11, 2004, 14:34:32
Job time : 51.2715 secs

```



ID AAY28871 standard; protein; 105 AA.  
 XX AC AAY28871;  
 XX DT 25-JAN-2000 (first entry)  
 XX DE Recombinant Met (-1) RaPLR1 GlnSer amino acid sequence.  
 XX KW Recombinant Met (-1) Rana pipiens ribonuclease GlnSer; RaPLR1; CD22;  
 KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;  
 KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;  
 KW recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;  
 KW autoimmune disease; RNase.  
 XX OS Rana pipiens.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 FT Misc-difference 1 /note= "Met not found in wild type RaPLR1"  
 FT Misc-difference 2 /note= "Wild type Gln replaced with Ser"  
 FT  
 XX WO9950398-A2.  
 XX PD 07-OCT-1999.  
 XX PF 26-MAR-1999; 99WO-US006641.  
 XX PR 27-MAR-1998; 98US-0079751P.  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX PI Rybak SM, Newton DL;  
 XX DR WPI; 1999-610847/52.  
 XX DR N-PSDB; AAZ08129.  
 XX New recombinant ribonucleases, used for killing target cells, e.g. for  
 PT treating cancers, viral infections or autoimmune diseases.  
 XX PS Claim 34; Page 61; 71pp; English.  
 XX The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1)  
 CC protein with Met at position 1 and Gln28Ser. Carboxy terminal end of  
 CC recombinant RaPLR1 has a covalently bound ligand binding moiety, which  
 CC can be a LL2 antibody directed against CD22 on cancerous B cells or human  
 CC chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.  
 CC Recombinant ribonucleases can be expressed in bacteria without an N-  
 CC terminal methionine due to the presence of a signal peptide that is  
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the  
 CC proteins to be fused in-frame with ligand binding moieties to form  
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and  
 CC autoimmune diseases  
 XX SQ Sequence 105 AA;  
 Query Match 46.7%; Score 280.5; DB 2; Length 105;  
 Best Local Similarity 49.5%; Pred. No. 3.9e-24;  
 Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;  
 QY 1 SNWATFQOKHIINT-PIICNTIMDNINIVGGQCKRVNTFISSATTVKAICTGVI-NMN 58  
 DB 2 SDWLTFFQKHLNTRDVCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 57  
 QY 59 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109  
 DB 58 VLTTFEFLSDC---NVTSRPCKYKLLKXSTNTFCVTCENQAPVHFVGVGHC 105  
 RESULT 11  
 AAY28865  
 ID AAY28865 standard; protein; 104 AA.

XX AAY28865;  
 XX AC 25-JAN-2000 (first entry)  
 XX DE Rana pipiens liver ribonuclease (RaPLR1).  
 XX KW Rana pipiens liver ribonuclease; RaPLR1; covalently bound; LL2 antibody;  
 KW ligand binding moiety; CD22; cancerous B cell; Kaposi's Sarcoma; frog;  
 KW human chorionic gonadotrophin; hCG; recombinant ribonuclease; RNase;  
 KW signal peptide; cytotoxic fusion protein; cancer; autoimmune disease.  
 XX OS Rana pipiens.  
 XX PN WO9950398-A2.  
 XX PD 07-OCT-1999.  
 XX PF 26-MAR-1999; 99WO-US006641.  
 XX PR 27-MAR-1998; 98US-0079751P.  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX PI Rybak SM, Newton DL;  
 XX DR WPI; 1999-610847/52.  
 XX DR N-PSDB; AAZ08124.  
 XX New recombinant ribonucleases, used for killing target cells, e.g. for  
 PT treating cancers, viral infections or autoimmune diseases.  
 XX PS Claim 1; Page 55; 71pp; English.  
 XX The present sequence is Rana pipiens liver ribonuclease (RaPLR1) protein.  
 CC Carboxy terminal end of RaPLR1 has a covalently bound ligand binding  
 CC moiety, which can be a LL2 antibody directed against CD22 on cancerous B  
 CC cells or human chorionic gonadotrophin (hCG) effective against Kaposi's  
 CC Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria  
 CC without an N-terminal methionine due to the presence of a signal peptide  
 CC that is cleaved by bacteria. The soluble expression of ribonuclease  
 CC allows the proteins to be fused in-frame with ligand binding moieties to  
 CC form cytotoxic fusion proteins. They can be used for treatment of cancer  
 CC and autoimmune diseases  
 XX SQ Sequence 104 AA;  
 Query Match 46.0%; Score 276.5; DB 2; Length 104;  
 Best Local Similarity 49.1%; Pred. No. 1.1e-23;  
 Matches 54; Conservative 15; Mismatches 32; Indels 9; Gaps 4;  
 QY 2 NWATFQOKHIINT-PIICNTIMDNINIVGGQCKRVNTFISSATTVKAICTGVI-NMN 59  
 DB 2 DWLTFQKHLNTRDVCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 57  
 QY 60 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109  
 DB 58 LTTSEFLSDC---NVTSRPCKYKLLKXSTNTFCVTCENQAPVHFVGVGHC 104  
 RESULT 12  
 AAY28867  
 ID AAY28867 standard; protein; 105 AA.  
 XX AC AAY28867;  
 XX DT 25-JAN-2000 (first entry)  
 XX DE Recombinant Met (-1) RaPLR1.  
 XX KW Recombinant Met (-1) Rana pipiens ribonuclease; RaPLR1; CD22; RNase;  
 KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;  
 KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;

**Qy**

60 LSTRFQLNCTRTSITPRPCPYSSRSTETNYICVKCENQVPHVFAGIGRC 109  
| : | : | : | : | : | : | : | : | : | : | : | : | : |  
| : | : | : | : | : | : | : | : | : | : | : | : | :

**Dd**

58 LTTFEFLSDC---NVTSRPCKYKLUKKSTNKFCVT'CNQAAPVHFVGVRGRC 104

AA28871



QY 2 NWATFQOKHIINTPIICNTIMDNIIYVGGQCKRVNTFIISATTVKAICTGVINMNVLS 61  
 Db 2 NWATFQOKHIINTPIICNTIMDNIIYVGGQCKRVNTFIISATTVKAICTGVINMNVLS 61  
 QY 62 TTRFOLNTCTRTSTITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
 Db 62 TTRFOLNTCTRTSTITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 6  
 AAY28876  
 ID AAY28876 standard; protein; 111 AA.  
 XX  
 AC  
 XX  
 DT  
 XX  
 DE  
 XX  
 KW Met (-1) Rana catesbeiana ribonuclease Met22Leu Met57Leu- (His)6; RaCOR1;  
 KW recombinant; CD22; covalently bound; LL2 antibody; ligand binding moiety;  
 KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;  
 KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;  
 KW cancer; bullfrog; RNase; autoimmune disease.  
 XX  
 OS Rana catesbeiana.  
 XX Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"  
 FT Misc-difference 1 /note= "(His)6 histidine tag attached to N-terminal Met"  
 FT Misc-difference 23 /note= "Wild type Met replaced with Leu"  
 FT Misc-difference 58 /note= "Wild type Met replaced with Leu"  
 FT  
 XX  
 FN WO9950398-A2.  
 XX  
 XX 07-OCT-1999.  
 XX  
 PF 26-MAR-1999; 99WO-US006641.  
 XX  
 PR 27-MAR-1998; 98US-0079751P.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Rybak SM, Newton DL;  
 XX  
 DR WPI; 1999-610847/52.  
 DR N-PSDB; AAZ08133.  
 XX  
 PT New recombinant ribonucleases, used for killing target cells, e.g. for  
 PT treating cancers, viral infections or autoimmune diseases.  
 XX  
 PS Claim 22; Page 66; 71pp; English.  
 XX  
 CC The present sequence is a recombinant Rana catesbeiana oocyte  
 CC ribonuclease (RaCOR1) protein with Met at position 1 attached to a (His)6  
 CC tag, Met23Leu and Met58Leu. Carboxy terminal end of recombinant RaCOR1  
 CC has a covalently bound ligand binding moiety, which can be a LL2 antibody  
 CC directed against CD22 on cancerous B cells or human chorionic  
 CC gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant  
 CC ribonucleases can be expressed in bacteria without an N-terminal  
 CC methionine due to the presence of a signal peptide that is cleaved by  
 CC bacteria. The soluble expression of ribonuclease allows the proteins to  
 CC be fused in-frame with ligand binding moieties to form cytotoxic fusion  
 CC proteins. They can be used for treatment of cancer and autoimmune  
 CC diseases  
 XX  
 SQ Sequence 111 AA;

Query Match 98.3%; Score 591; DB 2; Length 111;  
 Best Local Similarity 98.2%; Pred. No. 1.2e-59;  
 Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWATFQOKHIINTPIICNTIMDNIIYVGGQCKRVNTFIISATTVKAICTGVINMNVLS 61  
 Db 3 NWATFQOKHIINTPIICNTILDNIIYVGGQCKRVNTFIISATTVKAICTGVINMNVLS 62  
 QY 62 TTRFOLNTCTRTSTITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
 Db 63 TTRFOLNTCTRTSTITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 7  
 AAY33321  
 ID AAY33321 standard; protein; 111 AA.  
 XX  
 AC  
 XX  
 DT 29-NOV-1999 (first entry)  
 XX  
 DE Frog lectin protein fragment.  
 XX  
 KW Cytotoxic; RNase; ribonuclease; pancreatic; antibody; light chain;  
 KW heavy chain; cell surface marker; treatment; tumor; viral infection;  
 KW parasite infection; immune dysfunctional cell; autoimmune disease;  
 KW contraceptive; cell separation; transplantation; bone marrow ablation;  
 KW leukemia cell; T-cell; graft-versus-host disease; bullfrog; lectin.  
 XX  
 OS Rana catesbeiana.  
 XX  
 FN US9555073-A.  
 XX  
 PD 21-SEP-1999.  
 XX  
 PF 09-JUL-1997; 97US-00891848.  
 XX  
 PR 20-APR-1990; 90US-00510696.  
 PR 22-OCT-1991; 91US-00779195.  
 PR 04-FEB-1993; 93US-00014082.  
 PR 22-SEP-1993; 93US-00125462.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Rybak SM, Newton DL, Nicholls PJ, Youle RJ;  
 XX  
 DR WPI; 1999-560488/47.  
 XX  
 PT Recombinantly fused pancreatic RNase-targeting proteins useful for  
 PT treating tumors, infections, immune or autoimmune disorders and as a  
 PT contraceptive.  
 XX  
 PS Example 3; Fig 19; 47pp; English.  
 XX  
 CC This invention describes a novel nucleic acid construct comprising  
 CC sequences encoding functional pancreatic RNase and a second protein  
 CC (preferably the light and heavy chains of an antibody) which binds a  
 CC specific cell surface marker on a target cell and functions as a  
 CC cytotoxic agent. The products can be used for selectively killing cells  
 CC expressing a specific surface marker. They can be used for treating  
 CC tumors or infected cells (e.g. cells infected by viruses (especially  
 CC latent or chronic virus infections, such as human immunodeficiency virus  
 CC (HIV)-1, Epstein-Barr virus, herpes viruses (herpes simplex types 1 and  
 CC II), hepatitis viruses (B, non-A-non-B, and delta), herpes zoster,  
 CC cytomegalovirus)) and cells infected with parasites (such as the malaria  
 CC parasite)). They can also be used for treating immune dysfunctional cells  
 CC in immune and autoimmune diseases. Additionally, they may be used as  
 CC contraceptives. Finally they can also be used for cell separation in  
 CC vitro by selectively killing unwanted types of cells (e.g. in bone  
 CC marrow) prior to transplantation into a patient undergoing marrow  
 CC ablation by radiation or for killing leukemia cells or T-cells that would  
 CC cause graft-versus-host disease. This sequence represents a bullfrog

Query Match 99.3%; Score 597; DB 2; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-60; Mismatches 0; Indels 0; Gaps 0;  
 Matches 109; Conservative 0;

QY 2 NWATFQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61  
 DB 2 NWATFQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61  
 QY 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 110  
 DB 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 110

RESULT 4  
 AAY28873  
 ID AAY28873 standard; protein; 111 AA.

AC AAY28873;  
 XX  
 DT 25-JAN-2000 (first entry)  
 DE Recombinant Met (-1) RaCOR1.  
 XX Recombinant Met (-1) Rana catesbeiana oocyte ribonuclease; RaCOR1; CD22;  
 KW covalently bound; IL2 antibody; ligand binding moiety; cancerous B cell;  
 KW Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;  
 KW recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;  
 KW RNase; autoimmune disease.

OS Rana catesbeiana.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"  
 FT

XX WO9950398-A2.  
 XX 07-OCT-1999.  
 XX 26-MAR-1999; 99WO-US006641.  
 XX 27-MAR-1998; 98US-0079751P.  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX Rybak SM, Newton DL;  
 XX WPI; 1999-610847/52.  
 XX N-PSDB; AAZ08131.

XX New recombinant ribonucleases, used for killing target cells, e.g. for  
 PT treating cancers, viral infections or autoimmune diseases.  
 XX Claim 22; Page 63; 71pp; English.

XX The present sequence is a recombinant Rana catesbeiana oocyte  
 CC ribonuclease (RaCOR1) protein with Met at position 1. Carboxy terminal  
 CC end of recombinant RaCOR1 has a covalently bound ligand binding moiety,  
 CC which can be a IL2 antibody directed against CD22 on cancerous B cells or  
 CC human chorionic gonadotropin (hCG) effective against Kaposi's sarcoma  
 CC cells. Recombinant ribonucleases can be expressed in bacteria without an  
 CC N-terminal methionine due to the presence of a signal peptide that is  
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the  
 CC proteins to be fused in-frame with ligand binding moieties to form  
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and  
 CC autoimmune diseases

XX Sequence 111 AA;

Query Match 99.3%; Score 597; DB 2; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-60;

Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWATFQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61  
 DB 3 NWATFQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 62  
 QY 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 110  
 DB 63 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 111

RESULT 5  
 AAY28874  
 ID AAY28874 standard; protein; 110 AA.

AC AAY28874;  
 XX  
 DT 25-JAN-2000 (first entry)  
 DE Recombinant RaCOR1 Met22Leu Met57Leu amino acid sequence.  
 XX Recombinant Rana catesbeiana oocyte ribonuclease; covalently bound;  
 KW RaCOR1 Met22Leu Met57Leu; IL2 antibody; ligand binding moiety; CD22;  
 KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotropin; hCG;  
 KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;  
 KW cancer; bullfrog; RNase; autoimmune disease.  
 XX Rana catesbeiana.  
 OS Synthetic.

XX Key Location/Qualifiers  
 FH Misc-difference 22 /note= "Wild type Met replaced with Leu"  
 FT Misc-difference 57 /note= "Wild type Met replaced with Leu"  
 FT

XX WO9950398-A2.  
 XX 07-OCT-1999.  
 XX 26-MAR-1999; 99WO-US006641.  
 XX 27-MAR-1998; 98US-0079751P.  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX Rybak SM, Newton DL;  
 XX WPI; 1999-610847/52.  
 XX N-PSDB; AAZ08132.

XX New recombinant ribonucleases, used for killing target cells, e.g. for  
 PT treating cancers, viral infections or autoimmune diseases.  
 XX Claim 22; Page 64; 71pp; English.

XX The present sequence is a recombinant Rana catesbeiana oocyte  
 CC ribonuclease (RaCOR1) protein with Met22Leu Met57Leu. Carboxy terminal  
 CC end of recombinant RaCOR1 has a covalently bound ligand binding moiety, or  
 CC which can be a IL2 antibody directed against CD22 on cancerous B cells, or  
 CC human chorionic gonadotropin (hCG) effective against Kaposi's sarcoma  
 CC cells. Recombinant ribonucleases can be expressed in bacteria without an  
 CC N-terminal methionine due to the presence of a signal peptide that is  
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the  
 CC proteins to be fused in-frame with ligand binding moieties to form  
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and  
 CC autoimmune diseases

XX Sequence 110 AA;

Query Match 98.3%; Score 591; DB 2; Length 110;  
 Best Local Similarity 98.2%; Pred. No. 1.1e-59;  
 Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CC Recombinant ribonucleases can be expressed in bacteria without an N-  
 CC terminal methionine due to the presence of a signal peptide that is  
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the  
 CC proteins to be fused in-frame with ligand binding moieties to form  
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and  
 CC autoimmune diseases  
 XX  
 SQ Sequence 110 AA;

Query Match 100.0%; Score 601; DB 2; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 8.2e-61;  
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNWATFQOKHIIINTPIICNTIMDNNIYIVGGQCKRVNTFISSATVKAICTGVINMNVL 60  
 DB 1 SNWATFQOKHIIINTPIICNTIMDNNIYIVGGQCKRVNTFISSATVKAICTGVINMNVL 60

QY 61 STTRFQNLNCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
 DB 61 STTRFQNLNCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 2  
 AAY28878  
 ID AAY28878 standard; protein; 111 AA.  
 XX  
 AC AAY28878;  
 XX  
 DT 25-JAN-2000 (first entry)  
 XX  
 DE Recombinant Met(-1) RaCOR1 Gln1Ser amino acid sequence.  
 XX  
 KW Recombinant Met(-1) Rana catesbeiana oocyte ribonuclease Gln1Ser; RaCOR1;  
 KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;  
 KW Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;  
 KW recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;  
 KW CD22; RNase; autoimmune disease.  
 XX  
 OS Rana catesbeiana.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1  
 FT Misc-difference 2 /note= "Met not found in wild type RaCOR1"  
 FT Misc-difference 2 /note= "Wild type Gln replaced with Ser"  
 XX  
 PN WO9950398-A2.  
 XX  
 PD 07-OCT-1999.  
 XX  
 PF 26-MAR-1999; 99WO-US006641.  
 XX  
 PR 27-MAR-1998; 98US-0079751P.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Rybak SM, Newton DL;  
 XX  
 DR WPI; 1999-610847/52.  
 DR N-PSDB; AAZ08135.  
 XX  
 PT New recombinant ribonucleases, used for killing target cells, e.g. for  
 PT treating cancers, viral infections or autoimmune diseases.  
 XX  
 PS Claim 22; Page 68; 71pp; English.  
 XX  
 CC The present sequence is a recombinant Rana catesbeiana ribonuclease  
 CC (RaCOR1) protein with Met at position 1 and Gln2Ser. Carboxy terminal end  
 CC of recombinant RaCOR1 has a covalently bound ligand binding moiety, which  
 CC can be a LL2 antibody directed against CD22 on cancerous B cells or human  
 CC chorionic gonadotropin (hCG) effective against Kaposi's sarcoma cells.  
 CC Recombinant ribonucleases can be expressed in bacteria without an N-

CC terminal methionine due to the presence of a signal peptide that is  
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the  
 CC proteins to be fused in-frame with ligand binding moieties to form  
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and  
 CC autoimmune diseases  
 XX  
 SQ Sequence 111 AA;

Query Match 100.0%; Score 601; DB 2; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-61;  
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNWATFQOKHIIINTPIICNTIMDNNIYIVGGQCKRVNTFISSATVKAICTGVINMNVL 60  
 DB 2 SNWATFQOKHIIINTPIICNTIMDNNIYIVGGQCKRVNTFISSATVKAICTGVINMNVL 61

QY 61 STTRFQNLNCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
 DB 62 STTRFQNLNCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 3  
 AAY28872  
 ID AAY28872 standard; protein; 110 AA.  
 XX  
 AC AAY28872;  
 XX  
 DT 25-JAN-2000 (first entry)  
 XX  
 DE Rana catesbeiana oocyte ribonuclease (RaCOR1) amino acid sequence.  
 XX  
 KW Rana catesbeiana oocyte ribonuclease; RaCOR1; covalently bound; CD22;  
 KW LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's Sarcoma;  
 KW human chorionic gonadotropin; hCG; recombinant ribonuclease; bullfrog;  
 KW signal peptide; cytotoxic fusion protein; cancer; autoimmune disease;  
 KW RNase.  
 XX  
 OS Rana catesbeiana.  
 OS Synthetic.  
 XX  
 PN WO9950398-A2.  
 XX  
 PD 07-OCT-1999.  
 XX  
 PF 26-MAR-1999; 99WO-US006641.  
 XX  
 PR 27-MAR-1998; 98US-0079751P.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Rybak SM, Newton DL;  
 XX  
 DR WPI; 1999-610847/52.  
 DR N-PSDB; AAZ08130.  
 XX  
 PT New recombinant ribonucleases, used for killing target cells, e.g. for  
 PT treating cancers, viral infections or autoimmune diseases.  
 XX  
 PS Claim 22; Page 62; 71pp; English.  
 XX  
 CC The present sequence is a Rana catesbeiana oocyte ribonuclease (RaCOR1)  
 CC protein encoded by a cDNA modified for expression in E. coli. Carboxy  
 CC terminal end of RaCOR1 has a covalently bound ligand binding moiety,  
 CC which can be a LL2 antibody directed against CD22 on cancerous B cells or  
 CC human chorionic gonadotropin (hCG) effective against Kaposi's Sarcoma  
 CC cells. Recombinant ribonucleases can be expressed in bacteria without an  
 CC N-terminal methionine due to the presence of a signal peptide that is  
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the  
 CC proteins to be fused in-frame with ligand binding moieties to form  
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and  
 CC autoimmune diseases  
 XX  
 SQ Sequence 110 AA;

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 11, 2004, 14:23:43 ; Search time 50.2715 Seconds  
(without alignments)  
618.248 Million cell updates/sec

Title: US-09-961-400-24  
Perfect score: 601  
Sequence: 1 SNWATFQKHINTFLICNT.....ICVKENQYVHFAGIGRCP 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A.Geneseq 29Jan04: \*  
1: geneseqp1980s: \*  
2: geneseqp1980s: \*  
3: geneseqp2000s: \*  
4: geneseqp2001s: \*  
5: geneseqp2002s: \*  
6: geneseqp2003as: \*  
7: geneseqp2003bs: \*  
8: geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	601	100.0	110	2	AAY28877 Recombina
2	601	100.0	111	2	AAY28878 Recombina
3	597	99.3	110	2	AAY28872 Rana cate
4	597	99.3	111	2	AAY28873 Recombina
5	591	98.3	110	2	AAY28874 Recombina
6	591	98.3	111	2	AAY28876 Recombina
7	586.5	97.6	111	2	AAY33321 Frog lect
8	282.5	47.0	104	2	Aaw06544 Antitumou
9	280.5	46.7	104	2	AAY28870 Recombina
10	280.5	46.7	105	2	AAY28871 Recombina
11	276.5	46.0	104	2	AAY28865 Rana pipi
12	276.5	46.0	105	2	AAY28867 Recombina
13	276.5	46.0	112	2	Aaw35118 R. pipien
14	276.5	46.0	104	2	AAY28879 Rana pipi
15	276.5	46.0	251	2	Aaw35134 R. pipien
16	276.5	46.0	254	2	Aaw35135 R. pipien
17	276.5	46.0	355	2	Aaw35133 R. pipien
18	276.5	46.0	355	2	Aaw35129 R. pipien
19	276.5	46.0	366	2	Aaw35132 R. pipien
20	273.5	45.5	104	2	AAY28866 Recombina
21	273.5	45.5	105	2	AAY28869 Recombina
22	272.5	45.3	104	2	AAR12344 Protein w
23	272.5	45.3	104	2	AAR47303 ONCONASE
24	272.5	45.3	104	2	Aaw00736 Protein d
25	272.5	45.3	104	2	Aaw14065 Oncogene

ALIGNMENTS

RESULT 1

AAY28877

ID AAY28877 standard; protein; 110 AA.

XX

AC AAY28877;

XX

DT 25-JAN-2000 (first entry)

DE Recombinant RacOR1 Gln1Ser amino acid sequence.

XX

KW Recombinant Rana catesbeiana oocyte ribonuclease; RacOR1 Gln1Ser; CD22;

KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;

KW bullfrog; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; RNase;

KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;

KW cancer; autoimmune disease.

XX

OS Rana catesbeiana.

OS Synthetic.

XX

Key Location/Qualifiers

FT Misc-difference 1 /note= "Wild type Gln replaced with Ser"

FT

XX

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XX



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RA Beintema J.J.;
RT "secretory ribonuclease genes and pseudogenes in true ruminants.";
RL Gene 212:259-268(1998).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL; Y11670; CAA72368.1; -.
CC HSSP; P00656; ISRN.
CC InterPro; IPR001427; RNaseA.
CC Pfam; PF00074; rnaseA; 1.
CC PRINTS; PR00794; RIBONUCLEASE.
CC ProDom; PD000535; RNaseA; 1.
CC SMART; SM00092; RNasePc; 1.
CC PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
FT ACT SITE 41 41 BY SIMILARITY.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT CARBOHYD 62 62 N-LINKED (GLCNAC...) (BY SIMILARITY).
FT CARBOHYD 129 129 O-LINKED (BY SIMILARITY).
FT CARBOHYD 133 133 O-LINKED (BY SIMILARITY).
SQ SEQUENCE 151 AA; 16819 MW; E95F3757FFC5B233 CRC64;

Query Match 20.4%; Score 123.5; DB 1; Length 151;
Best Local Similarity 29.8%; Pred. No. 2.2e-06;
Matches 36; Conservative 18; Mismatches 44; Indels 23; Gaps 7;

Qy 5 ATFOCKHI-----INTPIICNTILDNNIYVGGOCKRVNTEFISSATTVAICTGVINL 58
Db 6 AKFRQHMADGSSSGNENYCNQMWR-RMTHGRCKPVNTEFVHESLDSVKAACS---QK 61

Qy 59 NVL-----STTRFQLNCTRTSITPRP-CFYSSRTETNYICVKCE-NQY-PVHFA 105
Db 62 NITCKNGQPNCVQSNSTWNITDCRETGSSKYPNCAKTSQKQKITVACEGNPYVPVHFD 121

Qy 106 G 106
Db 122 G 122

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Search completed: May 7, 2004, 21:53:06  
Job time : 5.60711 secs







DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).  
GN RNASE1 OR RNS1.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=70104197; PubMed=5460946;  
RA Jackson R.L., Hirs C.H.W.;  
RT "The primary structure of porcine pancreatic ribonuclease. II. The  
RT amino acid sequence of the reduced S-aminoethylated protein.";  
RL J. Biol. Chem. 245:637-653(1970).  
RN [2]  
RP REVISION TO 2.  
RA Wierenga R.K., Huizinga J.D., Gaastera W., Welling G.W., Beintema J.J.;  
RT "Affinity chromatography of porcine pancreatic ribonuclease and  
RT reinvestigation of the N-terminal amino acid sequence.";  
RL FEBS Lett. 31:181-185(1973).  
RN [3]  
RP DISULFIDE BONDS.  
RX MEDLINE=70104198; PubMed=4904878;  
RA Phelan J.J., Hirs C.H.W.;  
RT "The primary structure of porcine pancreatic ribonuclease. 3. The  
RT disulfide bonds.";  
RL J. Biol. Chem. 245:654-661(1970).  
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-  
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P  
CC with 2',3'-cyclic phosphate intermediates.  
CC -!- TISSUE SPECIFICITY: Pancreas.  
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
DR PIR; A92071; NSRG.  
DR HSSP; P00656; 1SRN.  
DR InterPro; IPR001427; RNaseA.  
DR Pfam; PF00074; RNaseA; 1.  
DR PRINTS; PR00794; RIBONUCLEASE.  
DR ProDom; PD000535; RNaseA; 1.  
DR SMART; SM00092; RNaseA; 1.  
DR PROSITE; PS00127; RNASE PANCREATIC; 1.  
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.  
FT DISULFID 26 84  
FT DISULFID 40 95  
FT DISULFID 58 110  
FT ACT SITE 12 12  
FT ACT SITE 12 12  
FT ACT SITE 41 41  
FT ACT SITE 119 119  
FT CARBOHYD 21 21  
FT CARBOHYD 34 34  
FT CARBOHYD 76 76  
SQ SEQUENCE 124 AA; 13804 MW; 0AC28CDE1411845 CRC64;  
Query Match 21.4%; Score 129.5; DB 1; Length 124;  
Best Local Similarity 30.7%; Pred No. 4.1e-07;  
Matches 35; Conservative 20; Mismatches 4; Indels 17; Gaps 6;  
Qy 7 PQKH-----INTPIICNTLDNIYVGGQCKRVNTFISSATTVKAICTGV-INLN 59  
Db 8 FORQHMDPDSSSSNSNYCNLMMSRR-NWTQGRCKFNTFVHESLADYQAVCSQINVNCK 66  
Qy 60 VLSITRFPNT-----CTRSITPRP-CPYSSRTETNYICVKCNQ--YVPHF 104  
Db 67 NGQTCNYQSNTMHTDCROTGSSKYPNCAYKASQEQKHIIIVACEGPNPVPVHF 120  
RESULT 10  
ENR\_BOVIN  
ID \_RNR\_BOVIN STANDARD; PRT; 167 AA.  
AC P39873;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Ribonuclease, brain precursor (EC 3.1.27.-) (BRB).  
GN BRN.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92093604; PubMed=1754384;  
RA Sasso M.P., Carsana A., Confalone E., Cosi C., Sorrentino S.,  
RA Viola M., Palmieri M., Russo E., Furia A.;  
RT "Molecular cloning of the gene encoding the bovine brain ribonuclease  
RT and its expression in different regions of the brain.";  
RL Nucleic Acids Res. 19:6469-6474(1991).  
RN [2]  
RP SEQUENCE OF 27-167, AND CARBOHYDRATE-LINKAGE SITES.  
RC TISSUE=Brain;  
RX MEDLINE=89214015; PubMed=3243767;  
RA Watanabe H., Katoh H., Ishii M., Komoda Y., Sanda A., Takizawa Y.,  
RA Ohgi K., Irie M.;  
RT "Primary structure of a ribonuclease from bovine brain.";  
RL J. Biochem. 104:939-945(1988).  
RN [3]  
RP SEQUENCE OF 27-167 FROM N.A.  
RX MEDLINE=96139017; PubMed=8587129;  
RA Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,  
RA Vento M.T., Furia A.;  
RT "Molecular evolution of genes encoding ribonucleases in ruminant  
RT species.";  
RL J. Mol. Evol. 41:850-858(1995).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
DR EMBL; X59767; CAA42439.1; -.  
DR EMBL; S81744; AAB36138.1; -.  
DR PIR; S20066; S20066.  
DR HSSP; P00656; 2RNS.  
DR GlycoSuiteDB; P39873; -.  
DR InterPro; IPR001427; RNaseA.  
DR Pfam; PF00074; RNaseA; 1.  
DR PRINTS; PR00794; RIBONUCLEASE.  
DR ProDom; PD000535; RNaseA; 1.  
DR SMART; SM00092; RNaseA; 1.  
DR PROSITE; PS00127; RNASE PANCREATIC; 1.  
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein; Signal.  
FT SIGNAL 1 26  
FT CHAIN 27 167 RIBONUCLEASE, BRAIN.  
FT ACT SITE 38 38 BY SIMILARITY.  
FT ACT SITE 67 67 BY SIMILARITY.  
FT ACT SITE 145 145 BY SIMILARITY.  
FT DISULFID 52 110 BY SIMILARITY.  
FT DISULFID 66 121 BY SIMILARITY.  
FT DISULFID 84 136 BY SIMILARITY.  
FT DISULFID 91 98 BY SIMILARITY.  
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .).  
FT CARBOHYD 155 155 /FTID=CAR\_000005.  
FT CARBOHYD 159 159 O-LINKED.  
FT CARBOHYD 155 155 O-LINKED.  
FT CONFLICT 155 155 T -> S (IN REF. 2).  
SQ SEQUENCE 167 AA; 18450 MW; 681CAAC3CC3FC459 CRC64;  
Query Match 21.4%; Score 129.5; DB 1; Length 167;  
Best Local Similarity 30.6%; Pred. No. 5.6e-07;





RL J. Biochem. 106:729-735 (1989).

CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-

CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P

CC with 2',3'-cyclic phosphate intermediates.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.

DR PIR: JX0085; JX0085.

DR HSP: P11916; IBC4.

DR InterPro: IPR001427; RNaseA.

DR Pfam: PF00074; RNaseA; 1.

DR ProDom: PD000535; RNaseA; 1.

DR SMART: SM00092; RNase\_Pc; 1.

DR PROSITE: PS00127; RNASE\_PANCREATIC; 1.

DR Hydrolase: Nuclease; Endonuclease; Pyrolidone carboxylic acid.

KW MOD\_RES 1 PYROLIDONE CARBOXYLIC ACID.

FT ACT\_SITE 10 10 BY SIMILARITY.

FT ACT\_SITE 35 35 BY SIMILARITY.

FT ACT\_SITE 104 104 BY SIMILARITY.

FT DISULFID 19 72 BY SIMILARITY.

FT DISULFID 34 82 BY SIMILARITY.

FT DISULFID 52 97 BY SIMILARITY.

FT DISULFID 94 111 PROBABLE.

SQ SEQUENCE 111 AA; 12461 MW; D64BA72456C10788 CRC64;

Query Match 61.2%; Score 370; DB 1; Length 111;

Best Local Similarity 64.9%; Pred. No. 4.4e-33;

Matches 72; Conservative 10; Mismatches 27; Indels 2; Gaps 2;

Qy 2 QNWATFOQKHINTPII-CNTILDNNIYVGQCKRVNTFISSATTVKAICTGVI-NLN 59

Db 1 QNMAKPEKHIRSTSSDCNTIMDKAIYVGCKKERNFTIISSEDNVKAICSGVSPDK 60

Qy 60 VLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 110

Db 61 ELSTTSFKLNTCIRDSITPRPCPYHSPDNKNKICVKCEKQLPVHFVGVGRC 111

RESULT 4

RN30\_RANPI STANDARD; PRT; 104 AA.

AC P22069;

DT 01-AUG-1991 (Rel. 19, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE P-30 protein (EC 3.1.27.-) (Onconase).

OS Rana pipiens (Northern leopard frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.

OX NCBI\_TaxID=8404;

RN [1]

RP TISSUE=Embryo;

RC MEDLINE=91093131; PubMed=1985896;

RA Ardelit W., Mikulski S.M., Shogen K.;

RT "Amino acid sequence of an anti-tumor protein from Rana pipiens

RT oocytes and early embryos. Homology to pancreatic ribonucleases."

RL J. Biol. Chem. 266:245-251 (1991).

RN [2]

RP 3D-STRUCTURE MODELING.

RC MEDLINE=93066156; PubMed=1438177;

RA Mosimann S.C., Johns K.L., Ardelit W., Mikulski S.M., Shogen K.,

RA James M.N.G.;

RT "Comparative molecular modeling and crystallization of P-30 protein:

RT a novel antitumor protein of Rana pipiens oocytes and early

RT embryos."

RL Proteins 14:392-400 (1992).

RN [3]

RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).

RC MEDLINE=94166079; PubMed=8120892;

RA Mosimann S.C., Ardelit W., James M.N.G.;

RT "Refined 1.7 A X-ray crystallographic structure of P-30 protein, an

RT amphibian ribonuclease with anti-tumor activity."

RL J. Mol. Biol. 236:1141-1153 (1994).

CC -1- FUNCTION: Basic protein with antiproliferative/cytotoxic activity

CC against several tumor cell lines in vitro, as well as antitumor

CC in vivo. It exhibits a ribonuclease-like activity against high

CC molecular weight ribosomal RNA.

CC -1- DEVELOPMENTAL STAGE: Early embryos (up to four blastomere stage).

CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.

DR PDB: 1ONG; 31-JAN-94.

DR InterPro: IPR001427; RNaseA.

DR Pfam: PF00074; RNaseA; 1.

DR ProDom: PD000535; RNaseA; 1.

DR SMART: SM00092; RNase\_Pc; 1.

DR PROSITE: PS00127; RNASE\_PANCREATIC; 1.

KW Hydrolase; Nuclease; Endonuclease; 3D-structure;

KW Pyrolidone carboxylic acid. PYROLIDONE CARBOXYLIC ACID.

FT MOD\_RES 1 1

FT ACT\_SITE 10 10

FT ACT\_SITE 31 31

FT ACT\_SITE 97 97

FT DISULFID 19 68

FT DISULFID 30 75

FT DISULFID 48 90

FT DISULFID 87 104

FT HELIX 3 10

FT STRAND 11 12

FT HELIX 19 22

FT TURN 23 24

FT TURN 26 30

FT STRAND 33 38

FT HELIX 41 45

FT HELIX 46 48

FT TURN 49 50

FT STRAND 55 58

FT STRAND 63 70

FT TURN 74 75

FT STRAND 77 84

FT STRAND 86 91

FT TURN 92 93

FT STRAND 94 101

SQ SEQUENCE 104 AA; 11845 MW; 22A753C2F9E566B4 CRC64;

Query Match 45.2%; Score 273.5; DB 1; Length 104;

Best Local Similarity 48.6%; Pred. No. 1e-22;

Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

Qy 2 QNWATFOQKHINT-PIICNTILDNNIYVGQCKRVNTFISSATTVKAICTGVI-NLN 59

Db 1 QDWLTFQKKHITNRDVCNIMTNLF---HCKDKNTFIYSRPEPVKAICKGILASKN 56

Qy 60 VLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 110

Db 57 VLTTFSEFVLSDC---NVTSRCKYKLLKSKTNKFCVTCENQAPVHFVGVGSC 104

RESULT 5

ANG3\_MOUSE STANDARD; PRT; 145 AA.

AC P97852;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Angiogenin-3 precursor (EC 3.1.27.-) (Angiogenin-related protein 2)

DE (EF-5).

GN ANG3 OR ANGL.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/c;

RX MEDLINE=97184476; PubMed=9032278;

RA Fu X., Kamps M.P.;

RT "E2a-Pbx1 induces aberrant expression of tissue-specific and



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:30:40 ; Search time 5.60711 seconds  
(without alignments)  
1030.796 Million cell updates/sec

Title: US-09-961-400-21

Perfect score: 605

Sequence: 1 MQNWATFQQRHIIPTIICN.....ICVKCENQYPVHFAGIGRCP 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	585.5	96.8	133	1	RNPO_RANCA
2	451	74.5	111	1	LECS_RANJA
3	370	61.2	111	1	RNPL_RANCA
4	273.5	45.2	104	1	RN30_RANPI
5	154.5	25.5	145	1	ANG3_MOUSE
6	149.5	24.7	145	1	ANGR_MOUSE
7	136.5	22.6	145	1	ANGI_MOUSE
8	131.5	21.7	124	1	RNP_BALAC
9	129.5	21.4	124	1	RNP_PIG
10	129.5	21.4	167	1	RNBR_BOVIN
11	127.5	21.1	119	1	RNP_IGUIG
12	124.5	20.6	151	1	RNBR_CAPCA
13	123.5	20.4	123	1	ANG2_BOVIN
14	123.5	20.4	141	1	RNBR_GIRCA
15	123.5	20.4	151	1	RNBR_AXIPR
16	123	20.3	146	1	ANGI_MIOTA
17	123	20.3	146	1	ANGI_SAIISC
18	120	19.8	146	1	ANGI_CERAE
19	120	19.8	147	1	ANGI_PONPY
20	119.5	19.8	143	1	RNBR_SHEEP
21	119	19.7	122	1	RNP_MACRU
22	118.5	19.6	123	1	ANGI_PIG
23	118.5	19.6	124	1	RNP_ANTAM
24	118	19.5	146	1	ANGI_AOTTR
25	117	19.3	146	1	ANGI_SAGOE
26	116.5	19.3	128	1	RNP_MYOCO
27	116.5	19.3	149	1	RNP_MOUSE
28	115	19.0	146	1	ANGI_MACMU
29	114.5	18.9	128	1	RNPB_CAVPO
30	114	18.8	148	1	ANGI_BOVIN
31	113.5	18.8	124	1	RNP_CAMDR
32	113.5	18.8	128	1	RNP_HORSE
33	113	18.7	147	1	ANGI_HUMAN

34	113	18.7	147	1	ANGI_PANTR
35	112.5	18.6	119	1	RNS4_BOVIN
36	112.5	18.6	128	1	RNP_PROGU
37	109.5	18.1	124	1	RNP_RANTA
38	109.5	18.1	146	1	ANGI_PAPHA
39	109.5	18.1	148	1	RNS4_MOUSE
40	109	18.0	125	1	ANGI_RABIT
41	108.5	17.9	124	1	RNP_CAPCA
42	108.5	17.9	124	1	RNP_GIRCA
43	108.5	17.9	130	1	RNP_CRILLO
44	107.5	17.8	124	1	RNP_BUBBU
45	107.5	17.8	148	1	RNP_PERLE

#### ALIGNMENTS

RESULT 1  
RNPO\_RANCA STANDARD; PRT; 133 AA.  
AC P11916; Q3PWR7;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ribonuclease, oocytes precursor (BC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SBL-C).  
DE binding lectin) (SBL-C).  
GN RCR.  
OS Rana catesbeiana (Bull frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
OX NCBI\_TaxID=8400;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=98165825; PubMed=9497370;  
RA Huang H.C., Wang S.C., Lu Y.J., Lu S.C., Liao Y.D.;  
RT "The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.  
RT Tissue distribution, cloning, purification, cytotoxicity, and active  
RT residues for RNase activity.";  
RL J. Biol. Chem. 273:6395-6401(1998).  
RN [2]  
RP SEQUENCE OF 23-133.  
RC TISSUE=Egg;  
RX MEDLINE=87299649; PubMed=3304421;  
RA Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,  
RT Takayanagi G., Hakomori S.;  
RT "Amino acid sequence of sialic acid binding lectin from frog (Rana  
RT catesbeiana) eggs.";  
RL Biochemistry 26:2189-2194(1987).  
RN [3]  
RP CHARACTERIZATION, AND SEQUENCE OF 81-101.  
RX MEDLINE=92220613; PubMed=1373237;  
RA Liao Y.-D.;  
RT "A pyrimidine-guanine sequence-specific ribonuclease from Rana  
RT catesbeiana (bullfrog) oocytes.";  
RL Nucleic Acids Res. 20:1371-1377(1992).  
RN [4]  
RP CHARACTERIZATION.  
RC TISSUE=Egg;  
RX MEDLINE=93192604; PubMed=8448385;  
RA Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,  
RT Takayanagi Y., Hakomori S., Titani K.;  
RT "Ribonuclease activity of sialic acid-binding lectin from Rana  
RT catesbeiana eggs.";  
RL Glycobiology 3:37-45(1993).  
RN [5]  
RP STRUCTURE BY NMR OF 23-133.  
RX MEDLINE=98437383; PubMed=9761686;  
RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;  
RT "The solution structure of a cytotoxic ribonuclease from the oocytes  
RT of Rana catesbeiana (bullfrog).";  
J. Mol. Biol. 283:231-244(1998).  
CC !- FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine

Q8wme8 pan troglod  
P15467 bos taurus  
P04059 proechimys  
P06666 rangifer ta  
Q8wn64 papio hamad  
Q91jhl mus musculus  
P31347 oryctolagus  
P06664 capreolus c  
P06662 giraffa cam  
P24717 cricetus  
P06657 bubalus bub  
Q9wuv5 peromyscus









```

Query Match          21.4%; Score 129.5; DB 2; Length 167;
Best Local Similarity 30.6%; Pred. No. 1e-05;
Matches 37; Conservative 18; Mismatches 43; Indels 23; Gaps

Qy 5 ATFOOKHI-----INTPIICNTILDNNIYIVGGCKRVNTFISSATTVKAICTGVINL 58
      ||::||: ||::||: ||::||: ||::||: ||::||: ||::||: ||::||: ||::||:
Db 32 AKFRQRMDSGSSSSPNYCMMKRR-RMTHGKCKPWNTFVHESLDDVKAVCS---OK 87
      ||::||: ||::||: ||::||: ||::||: ||::||: ||::||: ||::||: ||::||:
Qy 59 NVL-----STTFQLNCTRTSITPRP-CFYSSRTETNYICVKE-NQY-PVHFA 105
      ||::||: ||::||: ||::||: ||::||: ||::||: ||::||: ||::||: ||::||:
Db 88 NITCKNGHPNCYSKSTWSITDCRETGSSKYPNCAYKTSQOKYITVACEGNPYVPVHD 147
      ||::||: ||::||: ||::||: ||::||: ||::||: ||::||: ||::||: ||::||:
Qy 106 G 106
      |
Db 148 G 148

RESULT 9
S4111
C:Title: pancreatic ribonuclease - common iguana
C:Species: Iguana iguana (common iguana)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
C:Accession: S4111
R:Zhao, W.; Beintema, J.J.; Hofsteenge, J.
Eur. J. Biochem. 219, 641-646, 1994
A:Title: The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease
A:Reference number: S4111; MUID:94139745; PMID:8307028
A:Accession: S4111
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-119 <ZHA>
C:Superfamily: pancreatic ribonuclease

Query Match          21.1%; Score 127.5; DB 2; Length 119;
Best Local Similarity 29.6%; Pred. No. 1e-05;
Matches 34; Conservative 17; Mismatches 51; Indels 13; Gaps

Qy 2 QNWATFOOKHI-----INTPIICNTILDNNIYIVGGCKRVNTFISSATTVKAIC-- 52
      ||::||: ||::||: ||::||: ||::||: ||::||: ||::||: ||::||: ||::||:
Db 1 QDWSSFQNKHIDYPETGASNPAYCDLMMQRR-NLNPTKCKTRNTFVHASPSEIQQVCGS 59
      ||::||: ||::||: ||::||: ||::||: ||::||: ||::||: ||::||: ||::||:
Qy 53 --TGVINLVLSITTFEQLNCTRTSIT-PRCPYSSRTETNYICVKCNQYEVHF 104
      ||::||: ||::||: ||::||: ||::||: ||::||: ||::||: ||::||: ||::||:
Db 60 GGTHYEDNLXDSNESFDLTDCKNVGGTAPSSCKYNGTPTKRIACENNPQVHF 114
      ||::||: ||::||: ||::||: ||::||: ||::||: ||::||: ||::||: ||::||:

RESULT 10
NRKGR
Pancreatic ribonuclease (EC 3.1.27.5) - red kangaroo
N:Alternate names: RNase 1; RNase A
C:Species: Macropus rufus, Megaleia rufa (red kangaroo)
C>Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 04-Oct-1996
C:Accession: A00833
R:Gaastera, W.; Welling, G.W.; Beintema, J.J.
Eur. J. Biochem. 86, 209-217, 1978
A:Title: The amino-acid sequence of kangaroo pancreatic ribonuclease.
A:Reference number: A00833; MUID:78190621; PMID:658039
A:Accession: A00833
A:Molecule type: protein
A:Residues: 1-122 <GAA>
C:Superfamily: pancreatic ribonuclease
C:Keywords: Glycoprotein; Hydrolase; nucleic acid digestion; pancreas
F:11,40,117/Active site: His, Lys, His #status predicted
F:25-83,39-94,57-109,64-71/Bisulfide bonds: #status predicted
F:61/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match          19.7%; Score 119; DB 1; Length 122;
Best Local Similarity 29.8%; Pred. No. 8.2e-05;
Matches 34; Conservative 17; Mismatches 45; Indels 18; Gaps

Qy 7 FQOKHI-----INTPIICNTILDNNIYIVGGCKRVNTFISSATTVKAIC----- 52
      ||::||: ||::||: ||::||: ||::||: ||::||: ||::||: ||::||: ||::||:

```



GenCore version 5.1.6  
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OM protein - protein search, using sw model

```
Run on:      May  7, 2004, 21:38:36 ; Search time 10.072 Seconds
              (without alignments)
              1060.090 Million cell updates/sec
```

Title: US-09-961-400-21  
Perfect score: 605  
Sequence: 1 MQNWATFQOKHIINTPICN.....ICVKCENQYPVHFAGIGRCP 111

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues  
Total number of hits satisfying chosen parameters: 2833366

```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10
                  Listing first 45

```

```
Database : PIR_78:**
1: pir1:**
2: pir2:**
3: pir3:**
4: pir4:**
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match	Length				
1	582.5	96.3	111	2	A27121	1	ribonuclease-relat
2	451	74.5	111	2	JX0120	1	ribonuclease-relat
3	370	61.2	111	2	JX0085	1	pancreatic ribonuc
4	270.5	44.7	104	2	A39035	1	ribonuclease-relat
5	136.5	22.6	145	1	A39332	1	angiolegenin precurs
6	131.5	21.7	124	1	NRHK	1	pancreatic ribonuc
7	129.5	21.4	124	1	NRPG	1	pancreatic ribonuc
8	129.5	21.4	167	2	S20066	1	pancreatic-type ri
9	127.5	21.1	119	2	S41111	1	pancreatic ribonuc
10	119	19.7	122	1	NRXGR	1	pancreatic ribonuc
11	118.5	19.6	123	1	A43825	1	angiolegenin - pig
12	118.5	19.6	124	1	NRPRH	1	pancreatic ribonuc
13	116.5	19.3	128	1	NRUCU	1	pancreatic ribonuc
14	116.5	19.3	149	1	NRMS	1	pancreatic ribonuc
15	114.5	18.9	128	1	NRGPH	1	pancreatic ribonuc
16	114	18.8	125	1	A32474	1	angiolegenin [valida
17	113.5	18.8	124	1	NRCCM	1	pancreatic ribonuc
18	113.5	18.8	124	1	NRCCM	1	pancreatic ribonuc
19	113.5	18.8	124	1	NRCCB	1	pancreatic ribonuc
20	113.5	18.8	128	1	NRHO	1	pancreatic ribonuc
21	113	18.7	147	1	NRHUAG	1	angiolegenin precurs
22	112.5	18.6	128	1	NRXS	1	pancreatic ribonuc
23	110.5	18.3	124	2	S08549	1	ribonuclease - dom
24	109.5	18.1	124	1	NRDEN	1	pancreatic ribonuc
25	109	18.0	125	1	A43825	1	angiolegenin - rabbi
26	108.5	17.9	124	1	NRGFO	1	pancreatic ribonuc
27	108.5	17.9	124	1	NRDEO	1	pancreatic ribonuc
28	108.5	17.9	130	2	S22808	1	pancreatic ribonuc
29	107.5	17.8	124	1	NRWB	1	pancreatic ribonuc

## ALIGNMENTS

## RESULT 1

A27121  
ribonuclease-related sialic acid-binding lectin - bullfrog  
C/Species: Rana catesbeiana (bullfrog)  
C/Date: 13-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_c  
C/Accession: A27121  
R/Itami, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara  
Biochemistry 26, 2189-2194, 1987  
A/Title: Amino acid sequence of sialic acid-binding lectin  
A/Reference number: A27121; MUID:87299649; PMID:3304421  
A/Accession: A27121  
A/Molecule type: protein  
A/Residues: 1-111 <TIT>  
C/Superfamily: pancreatic ribonuclease  
C/Keywords: lectin

Query Match	96.3%	Score 582.5;	DB 2;	Length 111;
Best Local Similarity	96.4%;	Pred. No. 9.5e-51;		
Matches 107;	Conservative	3;	Mismatches 0;	Indels 1; Gaps 1;

  

Qy	2	QNWATPQOKHIIINTPII	-CNTILDNNIIYIVGGQCKRVNTFIISATTVKAICTGVINLV	60
Db	1	ENWATPQOKHIIINTPIINCNT	IMDNNIIYIVGGQCKRVNTFIISATTVKAICTGVINNV	60
Qy	61	LSSTRFQLNCTCTSI	TPRCPYSSSTETNYICVKENQYVHFAGIGRCP	111
Db	61	LSSTRFQLNCTCTSI	TPRCPYSSSTETNYICVKENQYVHFAGIGRCP	111

## RESULT 2

JX0120  
 ribonuclease-related sialic acid-binding lectin - Japanese frog  
 C;Species: Rana japonica (Japanese frog)  
 C;date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C;Accession: JX0120  
 R.;Kamiya, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawauchi, H.  
 J. Biochem. 108, 139-143, 1990  
 A.;Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica)  
 A.;Reference number: JX0120; MUID:91035319; PMID:2229005

Query Match 74.5%; Score 451; DB 1; Length 111;  
Best Local Similarity 77.5%; Pred. No. 1e-37;  
Matches 86: Conservative 8; Mismatches 15; Indels 2; Gaps 2;



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; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met22Leu and
; OTHER INFORMATION: Met57Leu substitutions (recombinant RaCOR1
; OTHER INFORMATION: Met22Leu Met57Leu)
US-09-948-391A-19

Query Match          98.2%; Score 594; DB 10; Length 110;
Best Local Similarity 99.1%; Pred. No. 1.3e-59;
Matches 109; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNLV 61
Db 1 QNWATFOQKHIIKTPICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNLV 60

Qy 62 STTRFQNLNCTRTSTTPRCPYSSRTETNYICVKCENQYPVHPAGIGRCP 111
Db 61 STTRFQNLNCTRTSTTPRCPYSSRTETNYICVKCENQYPVHPAGIGRCP 110

RESULT 13
US-09-948-391A-24
; Sequence 24, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Gln1ser substitution
; OTHER INFORMATION: (recombinant RaCOR1 Q1S)
US-09-948-391A-24

Query Match          97.7%; Score 591; DB 10; Length 110;
Best Local Similarity 98.2%; Pred. No. 2.9e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Qy 3 NWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNLV 62
Db 2 NWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNLV 61

Qy 63 TTRFQNLNCTRTSTTPRCPYSSRTETNYICVKCENQYPVHPAGIGRCP 111
Db 62 TTRFQNLNCTRTSTTPRCPYSSRTETNYICVKCENQYPVHPAGIGRCP 110

RESULT 14
US-09-961-400-24
; Sequence 24, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-24

Query Match          97.7%; Score 591; DB 10; Length 110;
Best Local Similarity 98.2%; Pred. No. 2.9e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNLV 62
Db 2 NWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNLV 61

Qy 63 TTRFQNLNCTRTSTTPRCPYSSRTETNYICVKCENQYPVHPAGIGRCP 111
Db 62 TTRFQNLNCTRTSTTPRCPYSSRTETNYICVKCENQYPVHPAGIGRCP 110

RESULT 15
US-09-961-400-9
; Sequence 9, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 111
; TYPE: PRT
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Db 1 QNWATFOQKHINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINMNV 60
Qy 62 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 9
US-09-948-391A-26
; Sequence 26, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1
; OTHER INFORMATION: and Gln2Ser substitution (Met(-1) RacOR1 QIS)
US-09-948-391A-26

Query Match 98.5%; Score 596; DB 10; Length 111;
Best Local Similarity 97.3%; Pred. No. 7.9e-60;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MOWWATFOQKHINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINLV 60
Db 1 MSNWATFOQKHINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINMV 60

Qy 61 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 10
US-09-961-400-26
; Sequence 26, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 26
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
; US-09-961-400-26

Query Match 98.5%; Score 596; DB 10; Length 111;
Best Local Similarity 97.3%; Pred. No. 7.9e-60;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MOWWATFOQKHINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINLV 60
Db 1 MSNWATFOQKHINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINMV 60

Qy 61 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 11
US-09-948-391A-17
; Sequence 17, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1
; OTHER INFORMATION: (recombinant Met(-1) RacOR1)
US-09-948-391A-17

Query Match 98.3%; Score 595; DB 10; Length 111;
Best Local Similarity 97.3%; Pred. No. 1e-59;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MOWWATFOQKHINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINLV 60
Db 1 MOWWATFOQKHINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINMV 60

Qy 61 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 12
US-09-948-391A-19
; Sequence 19, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
```

```

/ APPLICANT: Rybak, Susanna M.
/ APPLICANT: Newton, Dianne L.
/ APPLICANT: The United States of America
/ APPLICANT: as represented by The Secretary of the
/ APPLICANT: Department of Health and Human Services
/ TITLE OF INVENTION: Recombinant Anti-Tumor RNase
/ FILE REFERENCE: 015280-3431100S
/ CURRENT APPLICATION NUMBER: US/09/948,391A
/ CURRENT FILING DATE: 2002-05-10
/ PRIOR APPLICATION NUMBER: US 60/079,751
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: WO PCT/US99/06641
/ PRIOR FILING DATE: 1999-03-26
/ PRIOR APPLICATION NUMBER: US 09/622,613
/ PRIOR FILING DATE: 2000-08-17
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 15
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:Rana
/ OTHER INFORMATION: catesbeiana oocyte ribonuclease (RaCOR1) synthetic
/ OTHER INFORMATION: gene modified to use E. coli preferred codons
US-09-948-391A-15

Query Match          98.5%;   Score 596;   DB 10;   Length 110;
Best Local Similarity 98.2%;   Pred. No. 7.8e-60;
Matches 108;   Conservative 2;   Mismatches 0;   Indels 0;   Gaps

QY 2 QNWATFOQKHINTPIQNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNV
DB 1 QNWATFOQKHINTPIQNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNV
QY 62 STTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQPVHPAGIGRCP 111
DB 61 STTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQPVHPAGIGRCP 110

RESULT 8
US-09-961-400-15
/ Sequence 15, Application US/09961400
/ Publication No. US20030124131A1
/ GENERAL INFORMATION:
/ APPLICANT: RYBAK, SUSANNA M.
/ APPLICANT: GOLDENBERG, DAVID M.
/ APPLICANT: NEWTON, DIANNE L.
/ TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
/ TITLE OF INVENTION: CELLS
/ FILE REFERENCE: 018733/1059
/ CURRENT APPLICATION NUMBER: US/09/961,400
/ CURRENT FILING DATE: 2001-09-25
/ PRIOR APPLICATION NUMBER: 09/622,613
/ PRIOR FILING DATE: 2000-08-17
/ PRIOR APPLICATION NUMBER: PCT/US99/06641
/ PRIOR FILING DATE: 1999-03-26
/ PRIOR APPLICATION NUMBER: 60/079,751
/ PRIOR FILING DATE: 1998-03-26
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 15
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Rana catesbeiana
US-09-961-400-15

Query Match          98.5%;   Score 596;   DB 10;   Length 110;
Best Local Similarity 98.2%;   Pred. No. 7.8e-60;
Matches 108;   Conservative 2;   Mismatches 0;   Indels 0;   Gaps

QY 2 QNWATFOQKHINTPIQNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNV

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Db 1 MOWATFOOKHLINPTIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 60  
QY 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111  
Db 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 2  
US-09-961-400-21  
; Sequence 21, Application US/09961400  
; Publication No. US20030124131A1  
; GENERAL INFORMATION:  
; APPLICANT: RYBAK, SUSANNA M.  
; APPLICANT: GOLDENBERG, DAVID M.  
; APPLICANT: NEWTON, DIANNE L.  
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
; TITLE OF INVENTION: CELLS  
; FILE REFERENCE: 018733/1059  
; CURRENT APPLICATION NUMBER: US/09/961,400  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 60/079,751  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 111  
; TYPE: PRT  
; ORGANISM: Rana catesbeiana  
US-09-961-400-21

Query Match 100.0%; Score 605; DB 10; Length 111;  
Best Local Similarity 100.0%; Pred. No. 7.5e-61;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MOWATFOOKHLINPTIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 60  
Db 1 MOWATFOOKHLINPTIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 60  
QY 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111  
Db 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 3  
US-09-948-391A-22  
; Sequence 22, Application US/09948391A  
; Publication No. US20030027311A1  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: The United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase  
; FILE REFERENCE: 015280-343110US  
; CURRENT APPLICATION NUMBER: US/09/948,391A  
; CURRENT FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: US 60/079,751  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: US 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 117  
; TYPE: PRT

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Rana  
; OTHER INFORMATION: catesbeiana ribonuclease with (His)6 tag, Met at  
; OTHER INFORMATION: position 7, Met23Leu and Met58Leu substitutions  
; OTHER INFORMATION: (recombinant Met(-1) RacOR1 Met22Leu Met57Leu-(His)6)  
US-09-948-391A-22

Query Match 100.0%; Score 605; DB 10; Length 117;  
Best Local Similarity 100.0%; Pred. No. 8e-61;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MOWATFOOKHLINPTIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 60  
Db 7 MOWATFOOKHLINPTIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 66  
QY 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111  
Db 67 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117

RESULT 4  
US-09-961-400-22  
; Sequence 22, Application US/09961400  
; Publication No. US20030124131A1  
; GENERAL INFORMATION:  
; APPLICANT: RYBAK, SUSANNA M.  
; APPLICANT: GOLDENBERG, DAVID M.  
; APPLICANT: NEWTON, DIANNE L.  
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
; TITLE OF INVENTION: CELLS  
; FILE REFERENCE: 018733/1059  
; CURRENT APPLICATION NUMBER: US/09/961,400  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 60/079,751  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Rana catesbeiana  
US-09-961-400-22

Query Match 100.0%; Score 605; DB 10; Length 117;  
Best Local Similarity 100.0%; Pred. No. 8e-61;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MOWATFOOKHLINPTIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 60  
Db 7 MOWATFOOKHLINPTIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 66  
QY 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111  
Db 67 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117

RESULT 5  
US-09-961-400-17  
; Sequence 17, Application US/09961400  
; Publication No. US20030124131A1  
; GENERAL INFORMATION:  
; APPLICANT: RYBAK, SUSANNA M.  
; APPLICANT: GOLDENBERG, DAVID M.  
; APPLICANT: NEWTON, DIANNE L.  
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
; TITLE OF INVENTION: CELLS  
; FILE REFERENCE: 018733/1059  
; CURRENT APPLICATION NUMBER: US/09/961,400

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:40 ; Search time 35.6155 Seconds  
(without alignments)  
865.070 Million cell updates/sec

Title: US-09-961-400-21

Perfect score: 605

Sequence: 1 MNWATFOQKHIIPTICN.....ICVKCENQYPVHFAGIGRCP 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1140673 seqs, 277566755 residues

Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	605	100.0	111	10	US-09-948-391A-21
2	605	100.0	111	10	US-09-961-400-21
3	605	100.0	117	10	US-09-948-391A-22
4	605	100.0	117	10	US-09-961-400-22
5	601	99.3	111	10	US-09-961-400-17
6	600	99.2	110	10	US-09-961-400-19
7	596	98.5	110	10	US-09-948-391A-15
8	596	98.5	110	10	US-09-961-400-15
9	596	98.5	111	10	US-09-948-391A-26
10	596	98.5	111	10	US-09-961-400-26
11	595	98.3	111	10	US-09-948-391A-17
12	594	98.2	110	10	US-09-948-391A-19
13	591	97.7	110	10	US-09-948-391A-24
14	591	97.7	110	10	US-09-961-400-24
15	284.5	47.0	111	10	US-09-961-400-9

15 282.5 46.7 105 10 US-09-948-391A-6  
17 282.5 46.7 105 10 US-09-961-400-6  
18 281.5 46.5 105 10 US-09-961-400-8  
19 278.5 46.0 105 14 US-10-153-882-2  
20 277.5 45.9 104 10 US-09-961-400-2  
21 277.5 45.9 105 10 US-09-948-391A-13  
22 277.5 45.9 105 10 US-09-961-400-13  
23 277.5 45.9 127 10 US-09-948-391A-28  
24 277.5 45.9 127 10 US-09-961-400-28  
25 276.5 45.7 104 10 US-09-948-391A-2  
26 276.5 45.7 104 10 US-09-948-391A-4  
27 276.5 45.7 104 10 US-09-961-400-4  
28 272.5 45.0 104 10 US-09-948-391A-11  
29 272.5 45.0 104 10 US-09-961-400-11  
30 272.5 45.0 105 10 US-09-948-391A-8  
31 272.5 45.0 111 10 US-09-948-391A-9  
32 268.5 44.4 104 9 US-09-986-119-1  
33 268.5 44.4 104 10 US-09-918-887-1  
34 265.5 43.9 104 12 US-10-461-713-53  
35 202 33.4 83 9 US-09-986-119-3  
36 202 33.4 83 10 US-09-918-887-3  
37 161 26.6 169 13 US-10-016-447-2  
38 131.5 21.7 124 12 US-10-037-417-103  
39 127.5 21.1 119 12 US-10-016-248-89  
40 127.5 21.1 119 15 US-10-074-978A-139  
41 118 19.5 99 15 US-10-074-978A-141  
42 117 19.3 147 9 US-09-731-872-254  
43 117 19.3 147 10 US-09-876-997-254  
44 114 18.8 123 12 US-10-461-713-58  
45 114 18.8 124 13 US-10-016-447-5

#### ALIGNMENTS

#### RESULT 1

US-09-948-391A-21  
; Sequence 21, Application US/09948391A  
; Publication No. US20030027311A1  
; GENERAL INFORMATION:  
; APPLICANT: Rybak, Susanna M.  
; APPLICANT: Newton, Dianne L.  
; APPLICANT: The United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase  
; FILE REFERENCE: 015280-343110US  
; CURRENT APPLICATION NUMBER: US/09/948,391A  
; CURRENT FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: US 60/079,751  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: US 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 111  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Rana  
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1,  
; OTHER INFORMATION: Met21Leu and Met58Leu substitutions (recombinant  
; OTHER INFORMATION: Met(-1) RacOR1 Met22Leu Met57Leu)  
US-09-948-391A-21

Query Match 100.0%; Score 605; DB 10; Length 111;  
Best Local Similarity 100.0%; Pred. No. 7.5e-61;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 MNWATFOQKHIIPTICNTILDNIYIVGGQCKRVNTFISSATTVAICTGVINLV 60

APPLICANT: Wlodawer, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Paris, Susan K.  
REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 251 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-875-811-59

Query Match 45.2%; Score 273.5; DB 3; Length 251;  
Best Local Similarity 48.2%; Pred. No. 8.2e-24;  
Matches 54; Conservative 16; Mismatches 33; Indels 9; Gaps 4;

OY 1 MQNWATFQCKHLINT-PIICNTILDNNIYVGGQCKRVNTEILSSATTVKICTGVI-NL 58  
DB 147 MSDWLTFFQKHHITNTRDVCNIMSTNLF---HCKDKNTFYSRPEPVPKICKGIIASK 202

OY 59 NVLSTTRFQNTCTRTSITPRCPYSSRTETNYICVKCNQYVPVHFAGIGRC 110  
DB 203 NVLTTFSEFVLSDC--NVTSRPCKYKLLKSTNKFVCVCENQAPVHFVGVGSC 251

Search completed: May 7, 2004, 21:40:46  
Job time : 12.8756 secs



; MOLECULE TYPE: protein  
US-09-095-429-1

Query Match 45.2%; Score 273.5; DB 4; Length 104;  
Best Local Similarity 48.6%; Pred. No. 2.8e-24;  
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 2 QNWATFOOKHIINT-PIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVI-NLN 59

Db 1 QDWLTFQKKHINTNRDVCDCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 56

QY 60 VLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCNQYVPHFAGIGRC 110

Db 57 VLTTSEFYLSDC--NVTSPCKYKLLKSTNKFCVTCENQAPVHFVGVGSC 104

## RESULT 13

US-08-875-811-32

; Sequence 32, Application US/08875811

; Patent No. 6045793

; GENERAL INFORMATION:

; APPLICANT: Rybak, Susanna M.

; APPLICANT: Newton, Dianne L.

; APPLICANT: Boque, Lluis

; APPLICANT: Wlodawer, Alexander

; TITLE OF INVENTION: Recombinant Ribonuclease Proteins

; NUMBER OF SEQUENCES: 64

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/875,811

; FILING DATE: 19-FEB-1998

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US97/02588

; FILING DATE: 19-FEB-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/011,800

; FILING DATE: 21-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Paris, Susan K.

; REGISTRATION NUMBER: 41,739

; REFERENCE/DOCKET NUMBER: 015280-244100US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 32:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 112 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-875-811-32

Query Match 45.2%; Score 273.5; DB 3; Length 112;  
Best Local Similarity 48.2%; Pred. No. 3.1e-24;  
Matches 54; Conservative 16; Mismatches 33; Indels 9; Gaps 4;

QY 1 MQNWATFOOKHIINT-PIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVI-NL 58

Db 8 MSDWLTFQKKHINTNRDVCDCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASK 63

QY 59 NVLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCNQYVPHFAGIGRC 110

Db 64 NVLTTSEFYLSDC--NVTSPCKYKLLKSTNKFCVTCENQAPVHFVGVGSC 112

## RESULT 14

US-08-875-811-63

; Sequence 63, Application US/08875811

; Patent No. 6045793

; GENERAL INFORMATION:

; APPLICANT: Rybak, Susanna M.

; APPLICANT: Newton, Dianne L.

; APPLICANT: Boque, Lluis

; APPLICANT: Wlodawer, Alexander

; TITLE OF INVENTION: Recombinant Ribonuclease Proteins

; NUMBER OF SEQUENCES: 64

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/875,811

; FILING DATE: 19-FEB-1998

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US97/02588

; FILING DATE: 19-FEB-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/011,800

; FILING DATE: 21-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Paris, Susan K.

; REGISTRATION NUMBER: 41,739

; REFERENCE/DOCKET NUMBER: 015280-244100US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 63:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 129 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-875-811-63

Query Match 45.2%; Score 273.5; DB 3; Length 129;  
Best Local Similarity 48.6%; Pred. No. 3.7e-24;  
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 2 QNWATFOOKHIINT-PIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVI-NLN 59

Db 26 QDWLTFQKKHINTNRDVCDCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 81

QY 60 VLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCNQYVPHFAGIGRC 110

Db 82 VLTTSEFYLSDC--NVTSPCKYKLLKSTNKFCVTCENQAPVHFVGVGSC 129

## RESULT 15

US-08-875-811-59

; Sequence 59, Application US/08875811

; Patent No. 6045793

; GENERAL INFORMATION:

; APPLICANT: Rybak, Susanna M.

; APPLICANT: Newton, Dianne L.

; APPLICANT: Boque, Lluis

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Db 1 QDWLTFQKKHITNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56
QY 60 VLSTTRFOLNCTRTSITPRPCYPSSRTETNYICVKCENQYPVHFAGIGRC 110
Db 57 VLTTSEFVLSDC--NVTSRPCKYKLLKSTNKFVTCENQAPVHFVGVGSC 104

RESULT 10
US-09-687-748-2
; Sequence 2, Application US/09687748
; Patent No. 6423515
; GENERAL INFORMATION:
; APPLICANT: Saxena, Shaileendra K
; TITLE OF INVENTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
; FILE REFERENCE: 5013 US 01
; CURRENT APPLICATION NUMBER: US/09/687,748
; CURRENT FILING DATE: 2000-10-14
; PRIOR APPLICATION NUMBER: 09/394,268
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SEQ ID NO:1 with Leu at position 23 and Cys at
; OTHER INFORMATION: position 72
US-09-687-748-2

Query Match 45.2%; Score 273.5; DB 4; Length 104;
Best Local Similarity 43.5%; Pred. No. 2.8e-24;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 2 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NLN 59
Db 1 QDWLTFQKKHITNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56
QY 60 VLSTTRFOLNCTRTSITPRPCYPSSRTETNYICVKCENQYPVHFAGIGRC 110
Db 57 VLTTSEFVLSDC--NVTSRPCKYKLLKSTNKFVTCENQAPVHFVGVGSC 104

RESULT 11
US-08-626-288-1
; Sequence 1, Application US/08626288
; Patent No. 6649392
; GENERAL INFORMATION:
; APPLICANT: Youle, Richard
; APPLICANT: Vasandani, Veena
; APPLICANT: Wu, Yon-Neng
; APPLICANT: Boix, Ester
; APPLICANT: Ardelet, Wojciech
; TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which
; CURRENT APPLICATION DATA: Allows Production by Recombinant Methods
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/626,288
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/626,288
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ran, David B.
; REGISTRATION NUMBER: 38,589
; REFERENCE/DOCKET NUMBER: 15280-267
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
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```
; NAME: Ran, David B.
; REGISTRATION NUMBER: 38,589
; REFERENCE/DOCKET NUMBER: 15280-267
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-626-288-1

Query Match 45.2%; Score 273.5; DB 4; Length 104;
Best Local Similarity 48.6%; Pred. No. 2.8e-24;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 2 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NLN 59
Db 1 QDWLTFQKKHITNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56
QY 60 VLSTTRFOLNCTRTSITPRPCYPSSRTETNYICVKCENQYPVHFAGIGRC 110
Db 57 VLTTSEFVLSDC--NVTSRPCKYKLLKSTNKFVTCENQAPVHFVGVGSC 104

RESULT 12
US-09-095-429-1
; Sequence 1, Application US/09095429
; Patent No. 6649393
; GENERAL INFORMATION:
; APPLICANT: Youle, Richard
; APPLICANT: Vasandani, Veena
; APPLICANT: Wu, Yon-Neng
; APPLICANT: Boix, Ester
; APPLICANT: Ardelet, Wojciech
; TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which
; CURRENT APPLICATION DATA: Allows Production by Recombinant Methods
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,429
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/626,288
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ran, David B.
; REGISTRATION NUMBER: 38,589
; REFERENCE/DOCKET NUMBER: 15280-267
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
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APPLICANT: Wlodawer, Alexander  
TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588  
FILING DATE: 19-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/011,800  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Paris, Susan K.  
REGISTRATION NUMBER: 41,739  
REFERENCE/DOCKET NUMBER: 015280-244100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 358 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-875-811-51

Query Match 45.5%; Score 275.5; DB 3; Length 358;  
Best Local Similarity 48.2%; Pred. No. 7.5e-24;  
Matches 54; Conservative 17; Mismatches 32; Indels 9; Gaps 4;

Qy 1 MONWATFOOKHIINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NL 58  
Db 1 MEDWLTFOKKHITNTRDVCNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASK 56  
Qy 59 NVLSTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRC 110  
Db 57 VLTITSEFYLSDC---NVTSRCKYKLLKSTNKFCVTCENQAPVHFVGVGSC 105

RESULT 7  
US-09-394-268-1  
Sequence 1, Application US/09394268  
Patent No. 6175003  
GENERAL INFORMATION:  
APPLICANT: Saxena, Shailendra K  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF  
FILE OF INVENTION: MAKING THEM  
FILE REFERENCE: 5013  
CURRENT APPLICATION NUMBER: US/09/394,268  
CURRENT FILING DATE: 1999-09-10  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 104  
TYPE: PRT  
ORGANISM: Rana pipiens  
US-09-394-268-1

Query Match 45.2%; Score 273.5; DB 3; Length 104;

Best Local Similarity 48.6%; Pred. No. 2.8e-24;  
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;  
Qy 2 QNWATFOOKHIINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NLN 59  
Db 1 QDWLTFOKKHITNTRDVCNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASKN 56  
Qy 60 VLSTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRC 110  
Db 57 VLTITSEFYLSDC---NVTSRCKYKLLKSTNKFCVTCENQAPVHFVGVGSC 104

RESULT 8  
US-09-394-268-2  
Sequence 2, Application US/09394268  
Patent No. 6175003  
GENERAL INFORMATION:  
APPLICANT: Saxena, Shailendra K  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF  
FILE OF INVENTION: MAKING THEM  
FILE REFERENCE: 5013  
CURRENT APPLICATION NUMBER: US/09/394,268  
CURRENT FILING DATE: 1999-09-10  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 104  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: SEQ ID NO:1 with Leu at position 23 and Cys at  
OTHER INFORMATION: position 72  
US-09-394-268-2

Query Match 45.2%; Score 273.5; DB 3; Length 104;  
Best Local Similarity 49.5%; Pred. No. 2.8e-24;  
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

Qy 2 QNWATFOOKHIINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NLN 59  
Db 1 QDWLTFOKKHITNTRDVCNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASKN 56  
Qy 60 VLSTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRC 110  
Db 57 VLTITSEFYLSDC---NVTSRCKYKLLKSTNKFCVTCENQAPVHFVGVGSC 104

RESULT 9  
US-09-687-748-1  
Sequence 1, Application US/09687748  
Patent No. 6423515  
GENERAL INFORMATION:  
APPLICANT: Saxena, Shailendra K  
TITLE OF INVENTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES  
FILE OF INVENTION: 5013 US 01  
CURRENT APPLICATION NUMBER: US/09/687,748  
CURRENT FILING DATE: 2000-10-14  
PRIOR APPLICATION NUMBER: 09/394,268  
PRIOR FILING DATE: 1999-09-10  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 104  
TYPE: PRT  
ORGANISM: Rana pipiens  
US-09-687-748-1

Query Match 45.2%; Score 273.5; DB 4; Length 104;  
Best Local Similarity 48.6%; Pred. No. 2.8e-24;  
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

Qy 2 QNWATFOOKHIINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NLN 59





us-09-961-400-21.ra1

Sat May 8 17:57:20 2004

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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..111
; OTHER INFORMATION: /note= "Frog Lectin from Rana
; catesbeiana"
;
US-08-891-848-12
Query Match 96.3%; Score 582.5; DB 2; Length 111;
Best Local Similarity 96.4%; Pred. No. 5.9e-60;
Matches 107; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 2 QNWATFQOKHIINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVAICTGVINLV 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 ENWATFQOKHIINTPIINCNTIMDNNIYVGGQCKRVNTFISSATTVAICTGVINLV 60
QY 61 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 2
US-08-875-811-8
; Sequence 8, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..111
;

;
; OTHER INFORMATION: /note= "Frog Lectin from Rana
; catesbeiana"
;
US-08-875-811-8
Query Match 96.3%; Score 582.5; DB 3; Length 111;
Best Local Similarity 96.4%; Pred. No. 5.9e-60;
Matches 107; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 2 QNWATFQOKHIINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVAICTGVINLV 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 ENWATFQOKHIINTPIINCNTIMDNNIYVGGQCKRVNTFISSATTVAICTGVINLV 60
QY 61 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 3
US-08-467-955-2
; Sequence 2, Application US/08467955
; Patent No. 5728805
; GENERAL INFORMATION:
; APPLICANT: Ardelt Ph.D. Wojciech J.
; TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark H. Jay, P.A.
; STREET: P.O. Box E
; CITY: Short Hills
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07078-0383
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,955
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/178,118
; FILING DATE: 06-APR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/436,141
; FILING DATE: 13-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,332
; FILING DATE: 03-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,970
; FILING DATE: 01-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jay, Mark H.
; REGISTRATION NUMBER: 27507
; REFERENCE/DOCKET NUMBER: 5007 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-912-9066
; TELEFAX: 201-912-0442
; TELEX: No. 5728805 Applicable
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Rana pipiens
;

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GenCore version 5.1.6

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OM protein - protein search, using sw model

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Title: US-09-961-400-21

Perfect score: 605

Sequence: 1 MQNWTQQKHINTPICN.....ICVKENQYVHFAGIGRCP 111

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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	582.5	96.3	111	2	US-08-891-848-12
2	582.5	96.3	111	3	US-08-875-811-8
3	280.5	46.4	104	1	US-08-467-955-2
4	275.5	45.5	105	3	US-08-875-811-39
5	275.5	45.5	355	3	US-08-875-811-41
6	275.5	45.5	358	3	US-08-875-811-51
7	273.5	45.2	104	3	US-09-394-268-1
8	273.5	45.2	104	3	US-09-394-268-2
9	273.5	45.2	104	4	US-09-687-748-1
10	273.5	45.2	104	4	US-09-687-748-2
11	273.5	45.2	104	4	US-08-626-288-1
12	273.5	45.2	104	4	US-09-095-429-1
13	273.5	45.2	112	3	US-08-875-811-32
14	273.5	45.2	129	3	US-08-875-811-63
15	273.5	45.2	251	3	US-08-875-811-59
16	273.5	45.2	254	3	US-08-875-811-61
17	273.5	45.2	355	3	US-08-875-811-49
18	273.5	45.2	355	3	US-08-875-811-57
19	273.5	45.2	355	3	US-08-875-811-64
20	273.5	45.2	366	3	US-08-875-811-55
21	273.5	45.2	379	3	US-08-875-811-43
22	270.5	44.7	104	1	US-08-283-971-1
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24	270.5	44.7	104	1	US-08-467-955-1
25	270.5	44.7	104	1	US-08-891-848-13
26	270.5	44.7	104	4	US-08-626-288-2
27	270.5	44.7	104	4	US-09-095-429-2

28	268.5	44.4	104	3	US-08-875-811-1	Sequence 1, Appli
29	268.5	44.4	104	4	US-09-071-672-1	Sequence 1, Appli
30	268.5	44.4	104	4	US-09-986-119-1	Sequence 1, Appli
31	268.5	44.4	105	3	US-08-875-811-26	Sequence 26, Appl
32	268.5	44.4	106	3	US-08-875-811-28	Sequence 28, Appl
33	268.5	44.4	107	3	US-08-875-811-30	Sequence 30, Appl
34	267.5	44.2	105	3	US-08-875-811-30	Sequence 24, Appl
35	264.5	43.7	358	3	US-08-875-811-45	Sequence 45, Appl
36	264.5	43.7	365	3	US-08-875-811-53	Sequence 53, Appl
37	246.5	40.7	107	3	US-08-875-811-20	Sequence 20, Appl
38	235.5	38.9	111	3	US-08-875-811-22	Sequence 22, Appl
39	232	38.3	114	3	US-09-223-118-3	Sequence 22, Appl
40	228.5	37.8	360	3	US-08-875-811-47	Sequence 47, Appl
41	223	36.9	114	3	US-09-223-118-2	Sequence 2, Appli
42	222	36.7	114	3	US-09-223-118-1	Sequence 1, Appli
43	221	36.5	114	3	US-09-223-118-4	Sequence 4, Appli
44	202	33.4	83	3	US-08-875-811-2	Sequence 2, Appli
45	202	33.4	83	4	US-09-071-672-3	Sequence 3, Appli

## ALIGNMENTS

RESULT 1  
 US-08-891-848-12  
 ; Sequence 12, Application US/08891848  
 ; Patent No. 5955073  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rybak, Susanna M.  
 ; APPLICANT: Youle, Richard J.  
 ; APPLICANT: Newton, Dianne L.  
 ; APPLICANT: Nicholls, Peter J.  
 ; TITLE OF INVENTION: Selective RNase Cytotoxic Reagents  
 ; NUMBER OF SEQUENCES: 19  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, Eighth Floor  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94111-3834  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION NUMBER: US/08/891,848  
 ; FILING DATE: 22-SEP-1993  
 ; CLASSIFICATION: 530  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/125,462  
 ; FILING DATE: 22-SEP-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/014,082  
 ; FILING DATE: 04-FEB-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/779,195  
 ; FILING DATE: 22-OCT-1991  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/510,696  
 ; FILING DATE: 20-APR-1990  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Weber, Ellen Lauver  
 ; REGISTRATION NUMBER: 32,762  
 ; REFERENCE/DOCKET NUMBER: 015280-110310US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 576-0200  
 ; TELEFAX: (415) 576-0300  
 ; INFORMATION FOR SEQ ID NO: 12:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 111 amino acids  
 ; TYPE: amino acid



AC AAY39400;  
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 DT 01-DEC-1999 (first entry)  
 DE Recombinant frog Onconase.  
 DE Recombinant frog Onconase.  
 XX Ribonuclease; protein synthesis; inhibition; cancer; cytotoxic.  
 KW Rana pipiens.  
 OS  
 XX WO9946389-A1.  
 EN 16-SEP-1999.  
 PD  
 XX 11-MAR-1999; 99WO-US004252.  
 XX  
 PF 11-MAR-1998; 98US-0077557P.  
 XX  
 PR (IMMU-) IMMUNOMEDICS INC.  
 XX  
 PA Goldenberg DM, Hansen H, Leung S;  
 PI WPI; 1999-551416/46.  
 DR N-PSDB; AAZ19767.  
 DR  
 XX  
 PT A new recombinant Onconase used to treat, e.g. colon cancer.  
 PS Example 1; Fig 1; 42pp; English.  
 XX  
 CC This sequence represents recombinant frog Onconase. Onconase has  
 CC ribonuclease and anti-tumour activity. The cDNA was produced via PCR  
 CC (using primers AAZ19768-Z19769) of two synthetic DNAs whose sequences  
 CC encoded most of the N-terminal or the C-terminal amino acids of mature  
 CC Onconase. The two PCR products generated encoded either the N-terminal 54  
 CC amino acids (minus the initial methionine) or the C-terminal 51 amino  
 CC acids, and were ligated in frame at a NruI site. The cDNA was then  
 CC subcloned into a vector e.g., pBluescript, where the ATG initiation codon  
 CC was ligated to the cDNA. After expression in E. coli, the recombinant  
 CC protein was purified. The initial N-formyl methionine was cleaved off and  
 CC the new N-terminal glutamate residue cyclised to form an N-terminal  
 CC pyroglutamate. The pyroglutamate residue forms part of the phosphate  
 CC binding pocket of Onconase and is essential for both ribonuclease and anti-  
 CC -tumour activity. Onconase is a 12 kD ribonuclease which causes cell  
 CC death as a result of potent inhibition of protein synthesis by a  
 CC mechanism involving inactivation of cellular RNA. It is not inhibited by  
 CC mammalian placental ribonuclease inhibitor, which may explain its  
 CC enhanced cytotoxicity relative to mammalian enzymes. It has anti-tumour  
 CC activity against a variety of solid tumours e.g. colon or pancreatic  
 CC cancers, and can be used alone or in combination with other anti-cancer  
 CC agents such as tamoxifen. When used as an anti-tumour agent, Onconase can  
 CC be conjugated to a marker which targets it to a specific cell type  
 XX  
 SQ Sequence 105 AA;  
 Query Match 46.0%; Score 278.5; DB 2; Length 105;  
 Best Local Similarity 49.4%; Pred. No. 1.5e-23;  
 Matches 55; Conservative 16; Mismatches 32; Indels 9; Gaps 4;  
 QY 1 MQNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFTIISATVKAICTGVI-NLN 58  
 Db 1 MQWLTFOQKHINTKDVCDDNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIASK 56  
 QY 59 NVLSTTRFQNLNCTRTSITPRCPYSSRTETNYICVKCENQVPHFAGIGRC 110  
 Db 57 NVLTTSFYLSDC---NVTSRPCKYKLKSTNFKCTCENQAPVHFVGVGSC 105  
 RESULT 13  
 AAY28865  
 ID AAY28865 standard; protein; 104 AA.  
 XX  
 AC AAY28865;  
 XX

DT 25-JAN-2000 (first entry)  
 XX  
 DE Rana pipiens liver ribonuclease (RaPLR1).  
 XX  
 KW Rana pipiens liver ribonuclease; RaPLR1; covalently bound; LL2 antibody;  
 KW ligand binding moiety; CD22; cancerous B cell; Kaposi's Sarcoma; frog;  
 KW human chorionic gonadotrophin; hCG; recombinant ribonuclease; RNase;  
 KW signal peptide; cytotoxic fusion protein; cancer; autoimmune disease.  
 XX  
 OS Rana pipiens.  
 XX WO9950398-A2.  
 EN 07-OCT-1999.  
 PD  
 XX 26-MAR-1999; 99WO-US006641.  
 XX  
 PF 27-MAR-1998; 98US-0079751P.  
 XX  
 PR (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PA Rybak SM, Newton DL;  
 PI WPI; 1999-610847/52.  
 DR N-PSDB; AAZ08124.  
 DR  
 XX  
 PT New recombinant ribonucleases, used for killing target cells, e.g. for  
 PT treating cancers, viral infections or autoimmune diseases.  
 PS Claim 1; Page 55; 71pp; English.  
 XX  
 CC The present sequence is Rana pipiens liver ribonuclease (RaPLR1) protein.  
 CC Carboxy terminal end of RaPLR1 has a covalently bound ligand binding  
 CC moiety, which can be a LL2 antibody directed against CD22 on cancerous B  
 CC cells or human chorionic gonadotrophin (hCG) effective against Kaposi's  
 CC Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria  
 CC without an N-terminal methionine due to the presence of a signal peptide  
 CC that is cleaved by bacteria. The soluble expression of ribonuclease  
 CC allows the proteins to be fused in-frame with ligand binding moieties to  
 CC form cytotoxic fusion proteins. They can be used for treatment of cancer  
 CC and autoimmune diseases  
 XX  
 SQ Sequence 104 AA;  
 Query Match 45.9%; Score 277.5; DB 2; Length 104;  
 Best Local Similarity 48.6%; Pred. No. 1.9e-23;  
 Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;  
 QY 2 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFTIISATVKAICTGVI-NLN 59  
 Db 1 QDWLTFOQKHINTRDVCDDNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKN 56  
 QY 60 VLSTTRFQNLNCTRTSITPRCPYSSRTETNYICVKCENQVPHFAGIGRC 110  
 Db 57 VLTTSEFYLSDC---NVTSRPCKYKLKSTNFKCTCENQAPVHFVGVGHC 104  
 RESULT 14  
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 ID AAY28871 standard; protein; 105 AA.  
 XX  
 AC AAY28871;  
 XX  
 DT 25-JAN-2000 (first entry)  
 XX  
 DE Recombinant Met (-1) RaPLR1 Gln1Ser amino acid sequence.  
 XX  
 KW Recombinant Met (-1) Rana pipiens ribonuclease Gln1Ser; RaPLR1; CD22;  
 KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;  
 KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;  
 KW recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;  
 KW autoimmune disease; RNase.  
 XX



CC (Rana catesbeiana) lectin used to describe the method of the invention  
XX  
SQ Sequence 111 AA;

CC autoimmune diseases  
 XX Sequence 111 AA;  
 SQ

Query Match 98.5%; Score 596; DB 2; Length 111;  
 Best Local Similarity 97.3%; Pred. No. 1.9e-59;  
 Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGNWATFOQKHINTPIICNTILNNDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 60  
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 DB 1 MSNWATFOQKHINTPIICNTILNNDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60  
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QY 61 LSTTRFQLNTCTRTSIPTPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111  
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 DB 61 LSTTRFQLNTCTRTSIPTPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111  
 |||||

RESULT 6  
 AAY28877  
 ID AAY28877 standard; protein; 110 AA.  
 XX  
 AC AAY28877;  
 XX  
 DT 25-JAN-2000 (first entry)  
 XX  
 DE Recombinant RaCOR1 Gln1Ser amino acid sequence.  
 XX  
 KW Recombinant Rana catesbeiana oocyte ribonuclease; RaCOR1 Gln1Ser; CD22;  
 KW covalently bound; L12 antibody; ligand binding moiety; cancerous B cell;  
 KW bullfrog; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; RNase;  
 KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;  
 KW cancer; autoimmune disease.  
 XX  
 OS Rana catesbeiana.  
 OS Synthetic.  
 XX

Key Location/Qualifiers  
 FT Misc-difference 1 /note= "Wild type Gln replaced with Ser"  
 FT  
 FT WO9950398-A2.  
 PN  
 XX 07-OCT-1999.  
 PD  
 XX 26-MAR-1999; 99WO-US006641.  
 PF  
 XX 27-MAR-1998; 98US-0079751P.  
 PR  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA  
 XX Rybak SM, Newton DL;  
 XX WPI; 1999-610847/52.  
 DR N-P5DB; AAZ08134.  
 DR

New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.

Claim 22; Page 67; 71pp; English.

The present sequence is a recombinant Rana catesbeiana oocyte ribonuclease (RaCOR1) protein with Gln1Ser. Carboxy terminal end of recombinant RaCOR1 has a covalently bound ligand binding moiety, which can be a L12 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune diseases

XX Sequence 110 AA;  
 SQ

Query Match 97.7%; Score 591; DB 2; Length 110;  
 Best Local Similarity 98.2%; Pred. No. 6.8e-59;  
 Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 NWATFOQKHINTPIICNTILNNDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 62  
 |||||  
 DB 2 NWATFOQKHINTPIICNTILNNDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 61  
 |||||

QY 63 TTRFQLNTCTRTSIPTPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111  
 |||||  
 DB 62 TTRFQLNTCTRTSIPTPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
 |||||

RESULT 7  
 AAY33321  
 ID AAY33321 standard; protein; 111 AA.  
 XX  
 AC AAY33321;  
 XX  
 DT 29-NOV-1999 (first entry)  
 XX  
 DE Frog lectin protein fragment.  
 XX  
 KW Cytotoxic; RNase; ribonuclease; pancreatic; antibody; light chain;  
 KW heavy chain; cell surface marker; treatment; tumor; viral infection;  
 KW parasite infection; immune dysfunctional cell; autoimmune disease;  
 KW contraceptive; cell separation; transplantation; bone marrow ablation;  
 KW leukemia cell; T-cell; graft-versus-host disease; bullfrog; lectin.  
 XX  
 OS Rana catesbeiana.  
 XX  
 PN US5955073-A.  
 XX  
 PD 21-SEP-1999.  
 XX  
 PF 09-JUL-1997; 97US-00891848.  
 XX  
 PR 20-APR-1990; 90US-00510696.  
 PR 22-OCT-1991; 91US-00779195.  
 PR 04-FEB-1993; 93US-00014082.  
 PR 22-SEP-1993; 93US-00125462.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 XX Rybak SM, Newton DL, Nicholls PJ, Youle RJ;  
 XX WPI; 1999-560488/47.  
 XX

Recombinantly fused pancreatic RNase-targeting proteins useful for treating tumors, infections, immune or autoimmune disorders and as a contraceptive.

Example 3; Fig 19; 47pp; English.

This invention describes a novel nucleic acid construct comprising sequences encoding functional pancreatic RNase and a second protein (preferably the light and heavy chains of an antibody) which binds a specific cell surface marker on a target cell and functions as a cytotoxic agent. The products can be used for selectively killing cells expressing a specific surface marker. They can be used for treating tumors or infected cells (e.g. cells infected by viruses (especially latent or chronic virus infections, such as human immunodeficiency virus (HIV)-1, Epstein-Barr virus, herpes viruses (herpes simplex types I and II), hepatitis viruses (B, non-A-non-B, and delta), herpes zoster, cytomegalovirus) and cells infected with parasites (such as the malaria parasite)). They can also be used for treating immune dysfunctional cells in immune and autoimmune diseases. Additionally, they may be used as contraceptives. Finally they can also be used for cell separation in vitro by selectively killing unwanted types of cells (e.g. in bone marrow) prior to transplantation into a patient undergoing marrow ablation by radiation or for killing leukemia cells or T-cells that would cause graft-versus-host disease. This sequence represents a bullfrog

CC end of recombinant RaCOR1 has a covalently bound ligand binding moiety,  
 CC which can be a LL2 antibody directed against CD22 on cancerous B cells or  
 CC human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma  
 CC cells. Recombinant ribonucleases can be expressed in bacteria without an  
 CC N-terminal methionine due to the presence of a signal peptide that is  
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the  
 CC proteins to be fused in-frame with ligand binding moieties to form  
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and  
 CC autoimmune diseases

XX Sequence 110 AA;

Query Match 99.2%; Score 600; DB 2; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 6.5e-60;  
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QNWATFOOKHIIINTPIICNTILDNNIYVGGQCKRVNTFISSATTVAICTGVINLNL 61  
 Db 1 QNWATFOOKHIIINTPIICNTILDNNIYVGGQCKRVNTFISSATTVAICTGVINLNL 60  
 QY 62 STTRFQMLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111  
 Db 61 STTRFQMLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 4

AAZ28872  
 ID AAZ28872 standard; protein; 110 AA.

XX  
 AC AAZ28872;

XX 25-JAN-2000 (first entry)

XX Rana catesbeiana oocyte ribonuclease (RaCOR1) amino acid sequence.

XX Rana catesbeiana oocyte ribonuclease; RaCOR1; covalently bound; CD22;  
 KW LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's Sarcoma;  
 KW human chorionic gonadotrophin; hCG; recombinant ribonuclease; bullfrog;  
 KW signal peptide; cytotoxic fusion protein; cancer; autoimmune disease;  
 KW RNase.

XX Rana catesbeiana.  
 OS Synthetic.

XX WO9950398-A2.

XX 07-OCT-1999.

XX 26-MAR-1999; 99WO-US006641.

XX 27-MAR-1998; 98US-0079751P.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Rybak SM, Newton DL;

XX WPI; 1999-610847/52.

XX N-PSDB; AAZ08130.

XX New recombinant ribonucleases, used for killing target cells, e.g. for  
 PT treating cancers, viral infections or autoimmune diseases.

XX Claim 22; Page 62; 71pp; English.

XX The present sequence is a Rana catesbeiana oocyte ribonuclease (RaCOR1)  
 CC protein encoded by a cDNA modified for expression in E. coli. Carboxy  
 CC terminal end of RaCOR1 has a covalently bound ligand binding moiety,  
 CC which can be a LL2 antibody directed against CD22 on cancerous B cells or  
 CC human chorionic gonadotrophin (hCG) effective against Kaposi's Sarcoma  
 CC cells. Recombinant ribonucleases can be expressed in bacteria without an  
 CC N-terminal methionine due to the presence of a signal peptide that is  
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the  
 CC proteins to be fused in-frame with ligand binding moieties to form

CC cytotoxic fusion proteins. They can be used for treatment of cancer and  
 CC autoimmune diseases

XX Sequence 110 AA;

Query Match 98.5%; Score 596; DB 2; Length 110;  
 Best Local Similarity 98.2%; Pred. No. 1.8e-59;  
 Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QNWATFOOKHIIINTPIICNTILDNNIYVGGQCKRVNTFISSATTVAICTGVINLNL 61  
 Db 1 QNWATFOOKHIIINTPIICNTILDNNIYVGGQCKRVNTFISSATTVAICTGVINLNL 60  
 QY 62 STTRFQMLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111  
 Db 61 STTRFQMLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 5

AAZ28878  
 ID AAZ28878 standard; protein; 111 AA.

XX  
 AC AAZ28878;

XX 25-JAN-2000 (first entry)

XX Recombinant Met(-1) RaCOR1 Gln1Ser amino acid sequence.

XX Recombinant Met(-1) Rana catesbeiana oocyte ribonuclease Gln1Ser; RaCOR1;  
 KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;  
 KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;  
 KW recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;  
 KW CD22; RNase; autoimmune disease.

XX Rana catesbeiana.  
 OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"

FT Misc-difference 2 /note= "Wild type Gln replaced with Ser"

XX WO9950398-A2.

XX 07-OCT-1999.

XX 26-MAR-1999; 99WO-US006641.

XX 27-MAR-1998; 98US-0079751P.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Rybak SM, Newton DL;

XX WPI; 1999-610847/52.

XX N-PSDB; AAZ08135.

XX New recombinant ribonucleases, used for killing target cells, e.g. for  
 PT treating cancers, viral infections or autoimmune diseases.

XX Claim 22; Page 68; 71pp; English.

XX The present sequence is a recombinant Rana catesbeiana ribonuclease  
 CC (RaCOR1) protein with Met at position 1 and Gln2Ser. Carboxy terminal end  
 CC of recombinant RaCOR1 has a covalently bound ligand binding moiety, which  
 CC can be a LL2 antibody directed against CD22 on cancerous B cells or human  
 CC chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.  
 CC Recombinant ribonucleases can be expressed in bacteria without an N-  
 CC terminal methionine due to the presence of a signal peptide that is  
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the  
 CC proteins to be fused in-frame with ligand binding moieties to form  
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and



XX The present sequence is a recombinant Rana catesbeiana oocyte  
 CC ribonuclease (RaCOR1) protein with Met at position 1 attached to a (His)<sub>6</sub>  
 CC tag, Met23Leu and Met58Leu. Carboxy terminal end of recombinant RaCOR1  
 CC has a covalently bound ligand binding moiety, which can be a LL2 antibody  
 CC directed against CD22 on cancerous B cells or human chorionic  
 CC gonadotropin (hCG) effective against Kaposi's sarcoma cells. Recombinant  
 CC ribonucleases can be expressed in bacteria without an N-terminal  
 CC methionine due to the presence of a signal peptide that is cleaved by  
 CC bacteria. The soluble expression of ribonuclease allows the proteins to  
 CC be fused in-frame with ligand binding moieties to form cytotoxic fusion  
 CC proteins. They can be used for treatment of cancer and autoimmune  
 CC diseases  
 XX SQ Sequence 111 AA;  
 Query Match 100.0%; Score 605; DB 2; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-60;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MQNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVINLV 60  
 Db 1 MQNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVINLV 60  
 QY 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYVHFAGIGRCP 111  
 Db 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYVHFAGIGRCP 111  
 RESULT 2  
 AAY28873  
 ID AAY28873 standard; protein; 111 AA.  
 AC AAY28873;  
 XX 25-JAN-2000 (first entry)  
 DT Recombinant Met (-1) RaCOR1.  
 DE Recombinant Met (-1) RaCOR1.  
 XX Recombinant Met (-1) Rana catesbeiana oocyte ribonuclease; RaCOR1; CD22;  
 KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;  
 KW Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;  
 KW recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;  
 KW RNase; autoimmune disease.  
 XX Rana catesbeiana.  
 OS Synthetic.  
 XX Key Location/Qualifiers  
 FH Misc-difference 1 /note= "Met not found in wild type RaCOR1"  
 FT WO9950398-A2.  
 XX 07-OCT-1999.  
 XX 26-MAR-1999; 99WO-US006641.  
 XX 27-MAR-1998; 98US-0079751P.  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX Rybak SM, Newton DL;  
 XX WPI; 1999-610847/52.  
 XX N-PSDB; AAZ08131.  
 XX New recombinant ribonucleases, used for killing target cells, e.g. for  
 PT treating cancers, viral infections or autoimmune diseases.  
 XX Claim 22; Page 63; 71pp; English.  
 XX The present sequence is a recombinant Rana catesbeiana oocyte

CC ribonuclease (RaCOR1) protein with Met at position 1. Carboxy terminal  
 CC end of recombinant RaCOR1 has a covalently bound ligand binding moiety,  
 CC which can be a LL2 antibody directed against CD22 on cancerous B cells or  
 CC human chorionic gonadotropin (hCG) effective against Kaposi's sarcoma  
 CC cells. Recombinant ribonucleases can be expressed in bacteria without an  
 CC N-terminal methionine due to the presence of a signal peptide that is  
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the  
 CC proteins to be fused in-frame with ligand binding moieties to form  
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and  
 CC autoimmune diseases  
 XX SQ Sequence 111 AA;  
 Query Match 99.3%; Score 601; DB 2; Length 111;  
 Best Local Similarity 98.2%; Pred. No. 5e-60;  
 Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MQNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVINLV 60  
 Db 1 MQNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVINLV 60  
 QY 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYVHFAGIGRCP 111  
 Db 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYVHFAGIGRCP 111  
 RESULT 3  
 AAY28874  
 ID AAY28874 standard; protein; 110 AA.  
 AC AAY28874;  
 XX 25-JAN-2000 (first entry)  
 DT Recombinant RaCOR1 Met22Leu Met57Leu amino acid sequence.  
 DE Recombinant Rana catesbeiana oocyte ribonuclease; covalently bound;  
 KW RaCOR1 Met22Leu Met57Leu; LL2 antibody; ligand binding moiety; CD22;  
 KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotropin; hCG;  
 KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;  
 KW cancer; bullfrog; RNase; autoimmune disease.  
 XX Rana catesbeiana.  
 OS Synthetic.  
 XX Key Location/Qualifiers  
 FH Misc-difference 22 /note= "Wild type Met replaced with Leu"  
 FT Misc-difference 57 /note= "Wild type Met replaced with Leu"  
 FT WO9950398-A2.  
 XX 07-OCT-1999.  
 XX 26-MAR-1999; 99WO-US006641.  
 XX 27-MAR-1998; 98US-0079751P.  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX Rybak SM, Newton DL;  
 XX WPI; 1999-610847/52.  
 XX N-PSDB; AAZ08132.  
 XX New recombinant ribonucleases, used for killing target cells, e.g. for  
 PT treating cancers, viral infections or autoimmune diseases.  
 XX Claim 22; Page 64; 71pp; English.  
 XX The present sequence is a recombinant Rana catesbeiana oocyte  
 CC ribonuclease (RaCOR1) protein with Met22Leu Met57Leu. Carboxy terminal

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:25:55 ; Search time 47.3489 seconds  
(without alignments)  
662.376 Million cell updates/sec

Title: US-09-961-400-21

Perfect score: 605

Sequence: 1 MQNWATQKHINTPIQN.....TCVKCNGYPVHFAGIGRCP 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq\_29Jan04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	605	100.0	111	2	AAY28876
2	601	99.3	111	2	AAY28873
3	600	99.2	110	2	AAY28874
4	596	98.5	110	2	AAY28872
5	596	98.5	111	2	AAY28878
6	591	97.7	110	2	AAY28877
7	582.5	96.3	111	2	AAY28871
8	284.5	47.0	105	2	AAY28869
9	282.5	46.7	105	2	AAY28867
10	280.5	46.4	104	2	AAY28866
11	279.5	46.2	104	2	AAY28867
12	278.5	46.0	105	2	AAY28866
13	277.5	45.9	104	2	AAY28865
14	277.5	45.9	105	2	AAY28871
15	277.5	45.9	127	2	AAY28879
16	275.5	45.5	105	2	AAY28871
17	275.5	45.5	105	2	AAY28871
18	275.5	45.5	358	2	AAY28871
19	273.5	45.2	104	2	AAY28871
20	273.5	45.2	104	4	AAB31667
21	273.5	45.2	104	4	AAB31666
22	273.5	45.2	104	4	AAB31666
23	273.5	45.2	104	5	ABG32650
24	273.5	45.2	112	2	AAY28871
25	273.5	45.2	251	2	AAY28871

26	273.5	45.2	254	2	AAW35135
27	273.5	45.2	355	2	AAW35133
28	273.5	45.2	355	2	AAW35129
29	273.5	45.2	366	2	AAW35132
30	273.5	45.2	379	2	AAW35126
31	272.5	45.0	104	2	AAW30302
32	272.5	45.0	104	2	AAI28870
33	270.5	44.7	104	2	AAI28870
34	270.5	44.7	104	2	AAI28870
35	270.5	44.7	104	2	AAW00736
36	270.5	44.7	104	2	AAW14065
37	270.5	44.7	104	2	AAW06543
38	270.5	44.7	104	2	AAW88233
39	270.5	44.7	104	2	AAW88233
40	268.5	44.4	105	2	AAW35116
41	268.5	44.4	106	2	AAW35116
42	268.5	44.4	107	2	AAW35117
43	267.5	44.2	105	2	AAW35115
44	264.5	43.7	358	2	AAW35127
45	264.5	43.7	365	2	AAW35131

## ALIGNMENTS

### RESULT 1

AAI28876	AAI28876	standard; protein; 111 AA.
XX	AC	
XX	AAI28876;	
XX	25-JAN-2000	(first entry)
XX	Recombinant Met (-1) RaCOR1 Met22Leu Met57Leu- (His)6 protein.	
XX	Met (-1) Rana catesbeiana ribonuclease Met22Leu Met57Leu- (His)6; RaCOR1; recombinant; CD22; covalently bound; Lf2 antibody; ligand binding moiety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog; RNase; autoimmune disease.	
XX	Rana catesbeiana.	
OS	Synthetic.	
XX		
XX	Key	Location/Qualifiers
FT	Misc-difference 1	/note= "Met not found in wild type RaCOR1"
FT	Misc-difference 1	/note= "(His)6 histidine tag attached to N-terminal Met"
FT	Misc-difference 23	/note= "Wild type Met replaced with Leu"
FT	Misc-difference 58	/note= "Wild type Met replaced with Leu"
XX	WO9950398-A2.	
XX	07-OCT-1999.	
XX	26-MAR-1999;	99WO-US006641.
XX	27-MAR-1998;	98US-0079751P.
XX	(USSH ) US DEPT HEALTH & HUMAN SERVICES.	
XX	Rybak SM, Newton DL;	
XX	WPI; 1999-610847/52.	
XX	N-PSDB; AA208133.	
XX	New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.	
XX	Claim 22; Page 66; 71pp; English.	

RA Beintema J.J.;  
RT "Secretory ribonuclease genes and pseudogenes in true ruminants.";  
RL Gene 212.259-268(1998).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; Y11670; CAA72368.1; -;  
DR HSP; P00656; ISRN.  
DR InterPro; IPR001427; RNaseA.  
DR Pfam; PF00074; RNaseA; 1.  
DR PRINTS; PR00794; RIBONUCLEASE.  
DR ProDom; PD000535; RNaseA; 1.  
DR SMART; SM00092; RNase PC; 1.  
DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.  
FT ACT SITE 41 41 BY SIMILARITY.  
FT DISULFID 26 84 BY SIMILARITY.  
FT DISULFID 40 95 BY SIMILARITY.  
FT DISULFID 58 110 BY SIMILARITY.  
FT DISULFID 65 72 BY SIMILARITY.  
FT CARBOHYD 62 62 N-LINKED (GLCNAC...) (BY SIMILARITY).  
FT CARBOHYD 129 129 O-LINKED (BY SIMILARITY).  
FT CARBOHYD 133 133 O-LINKED (BY SIMILARITY).  
SQ SEQUENCE 151 AA; 16819 MW; E95F3757FPC5B233 CRC64;

Query Match 20.6%; Score 123.5; DB 1; Length 151;  
Best Local Similarity 29.8%; Pred. No. 2.2e-06;  
Matches 36; Conservative 18; Mismatches 44; Indels 23; Gaps 7;

Qy 4 ATFOQKH-----INTPLICNTLDNNIYVGGCKRVNTFISSATTVAICTGVNL 57  
Db 6 AKFRQHDAGSSSGNSGNYCNQMMKRR-RMTHGRCKPNTFVHESLDSVKAACS---QK 61  
Qy 58 NVL-----STTRFQNTCTRTSITPRP-CFYSSRTETNYICVKE-NOY-PVHFA 104  
Db 62 NITCKNGQPCVQSNSTWNITDCRETGSSKYPNCAYKTSQKQYITVACEGNPYVPHFD 121  
Qy 105 G 105  
Db 122 G 122

Search completed: May 7, 2004, 21:53:06  
Job time : 5.55659 secs



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OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OX Bovidae; Bovinae; Bos.
RN NCBI_TaxID=9913;
[1]
RN SEQUENCE.
RC TISSUE=Milk, and Serum;
RX MEDLINE=97409980; PubMed=9266695;
RA Strydom D.J., Bond M.D., Vallee B.L.;
RT "An angiogenic protein from bovine serum and milk -- purification and
primary structure of angiogenin-2.";
RL Eur. J. Biochem. 247:535-544 (1997).
CC -!- FUNCTION: Binds tightly to placental ribonuclease inhibitor and
has very low ribonuclease activity. Has potent angiogenic
activity. Angiogenin induces vascularization of normal and
malignant tissues. Abolishes protein synthesis by specifically
hydrolyzing cellular tRNAs.
CC -!- TISSUE SPECIFICITY: Serum and milk.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR HSP; P10152; IAGI.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.
DR PRINTS; PR00794; RIBONUCLEASE.
DR PRODOM; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW Protein synthesis inhibitor; Glycoprotein;
KW Pyridoxone carboxylic acid. PYROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 1
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 39 39 BY SIMILARITY.
FT ACT_SITE 113 113 BY SIMILARITY.
FT DISULFID 25 80
FT DISULFID 38 91
FT DISULFID 56 106
FT CARBOHYD 33 33 N-LINKED (GLCNAC...).
SQ SEQUENCE 123 AA; 14522 MW; B703B9839919FD2F CRC64;

Query Match 20.6%; Score 123.5; DB 1; Length 123;
Best Local Similarity 29.6%; Pred. No. 1.8e-06;
Matches 32; Conservative 20; Mismatches 43; Indels 13; Gaps 5;

Oy 6 FQKHINTPT-----ICNTILDNNIYVGQCKRVNTEFISSATTVKAIC---TGVINL 57
Db 8 FLRKHYPSPGTHDDRYCNYTWERR--NMTRPKDNTNFIHNSDDIRAVCDRNGEPYR 65

Oy 58 NVLSTTR--FQNTCTRTSITPR-PCPYSSRTETNYICVKCEQYPVH 102
Db 66 NGLRRSRSPFQVTTCTHRHGGSPPCRYRFRANRVIVIRCDDGFPPIH 113

RESULT 14
RNBR_GIRCA STANDARD; PRT; 141 AA.
AC Q29542; Q29533;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ribonuclease, brain (EC 3.1.27.-) (BRB).
GN BRN.
OS Giraffa camelopardalis (Giraffe).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Giraffoidea;
OC Giraffidae; Giraffa.
OX NCBI_TaxID=9894;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96139017; PubMed=8587129;
RA Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
RA Vento M.T., Furia A.;
RT "Molecular evolution of genes encoding ribonucleases in ruminant
species.";
RL J. Mol. Evol. 41:850-858 (1995).

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RN SEQUENCE OF 31-114 FROM N.A.
RX MEDLINE=93367815; PubMed=8360916;
RA Breukelman H.J., Beintema J.J., Confalone E., Costanzo C., Sasso M.P.,
RA Carsana A., Palmieri M., Furia A.;
RT "Sequences related to the ox pancreatic ribonuclease coding region in
the genomic DNA of mammalian species.";
RL J. Mol. Evol. 37:29-35 (1993).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
CC EMBL; S81743; AAB36137.1; -.
CC EMBL; S65126; AAB27931.1; -.
CC HSP; P00656; 2RNS.
CC InterPro: IPR001427; RNaseA.
CC Pfam: PF00074; RNaseA; 1.
CC PRINTS; PR00794; RIBONUCLEASE.
CC PRODOM; PD000535; RNaseA; 1.
CC SMART; SM00092; RNaseA; 1.
CC PROSITE; PS00127; RNASE PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT ACT_SITE 41 41 BY SIMILARITY.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT CARBOHYD 62 62 N-LINKED (GLCNAC... (BY SIMILARITY).
FT CARBOHYD 129 129 O-LINKED (BY SIMILARITY).
SQ SEQUENCE 141 AA; 15592 MW; 73745EFE9079591F CRC64;

Query Match 20.6%; Score 123.5; DB 1; Length 141;
Best Local Similarity 29.8%; Pred. No. 2.1e-06;
Matches 36; Conservative 18; Mismatches 44; Indels 23; Gaps 7;

Oy 4 ATFOOKHI-----INTPIICNTILDNNIYVGQCKRVNTEFISSATTVKAICTGVINL 57
Db 6 AKFRHMDHSGSSSSSSNSNYCNQMKR-RWTHRCAPVNTFVHESLADYKAVCS---QK 61

Oy 58 NVL-----STTRFQNTCTRTSITPR-CPYSSRTETNYICVKCE-NQY-PVHFA 104
Db 62 NITCKNGQPCYQSNSTMTNITDCRETGSSKYPNCAYKTSOKQYITVACGPNYPVPHFD 121

Oy 105 G 105
Db 122 G 122

RESULT 15
RNBR_AXIPR STANDARD; PRT; 151 AA.
AC P87350;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease, brain (EC 3.1.27.-) (BRB).
GN BRN.
OS Axis porcinus (Hog deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
OC Cervidae; Cervinae; Axis.
OX NCBI_TaxID=57737;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98278842; PubMed=9611269;
RA Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,

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Matches 37; Conservative 18; Mismatches 43; Indels 23; Gaps 7;

QY 4 ATFOOKHI-----INTPIICNTILDNNIYIVGGCKRVNFTFISSATTVKAICTGVINL 57  
DB ::::  
32 AKFERQHMDSGSSSSSPENYCQMKKR-RMTHGRCFVNFTFHESLDDVKAVCS---QK 87

QY 58 NVL-----STTFQLNCTRTTITRRP-CFYSSRTETNYICVKCE-NQY-PVHFA 104  
DB :  
88 NITCKNGHPNCYSQSKSTSIITDRETGSYPNCAYTSQKYITVACEGNPVVPVHF 147

QY 105 G 105  
DB 148 G 148

RESULT 11  
RNP\_IGUIG STANDARD; PRT; 119 AA.  
AC P80287;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Ribonuclease pancreatic [EC 3.1.27.5] (RNase 1) (RNase A).  
OS Iguana iguana (Common iguana).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.  
OX NCBI\_TaxID=9517;  
FN [1]  
RP SEQUENCE.

CC CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.  
CC CC -1- SUBCELLULAR LOCATION: Secreted.  
CC CC -1- TISSUE SPECIFICITY: Pancreas.  
CC CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
DR PR; S4111; S4111.  
DR HSP; P00656; ILSQ.  
DR InterPro; IPR001427; RNaseA.  
DR Pfam; PF00074; rnaseA; 1.  
DR PRINTS; PR00794; RIBONUCLEASE.  
DR ProDom; PD000535; RNaseA; 1.  
DR SMART; SM00092; RNase\_Pc; 1.  
DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
KW Hydrolase; Nuclease; Endonuclease; Pyrididone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT FT DISULFID 25 80 BY SIMILARITY.  
FT FT DISULFID 39 91 BY SIMILARITY.  
FT FT DISULFID 57 106 BY SIMILARITY.  
FT FT ACT\_SITE 10 10 BY SIMILARITY.  
FT FT ACT\_SITE 40 40 BY SIMILARITY.  
FT FT ACT\_SITE 113 113 BY SIMILARITY.  
SQ SEQUENCE 119 AA; 13324 MW; 6072FB5B7B15BD5A CRC64;

Query Match 21.2%; Score 127.5; DB 1; Length 119;  
Best Local Similarity 29.6%; Pred.No. 6.5e-07;  
Matches 34; Conservative 17; Mismatches 51; Indels 13; Gaps 4;

QY 1 QNWATFOOKHI-----INTPIICNTILDNNIYIVGGCKRVNFTFISSATTVKAIC-- 51  
DB :  
1 QDWSSFQNKHIDYPETSASNPAYCDLMWQR-NLNPTKCYTRVTFPHASPEIQQVCGS 59

QY 52 --TGVINLVSTTFPLNTCRISIT-PRCPYSSRTETNYICVKCENQYPVHF 103  
DB :  
60 GGTHVEDNLSDNESFDLTDCKNVGSTAPSSCKYNGTPGTKRIIRACENNQPVHF 114

RESULT 12

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DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.1.27.5) (RNase 1) (RNase A).
GN RNASE1 OR RNS1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=70104197; PubMed=5460946;
RA Jackson R.L., Hirs C.H.W.;
RT "The primary structure of porcine pancreatic ribonuclease. II. The
RT amino acid sequence of the reduced S-aminoethylated protein.";
RL J. Biol. Chem. 245:637-653 (1970).
RN [2]
RP REVISION TO 2.
RA Wierenga R.K., Huisinga J.D., Gastra W., Welling G.W., Beintema J.J.;
RT "Affinity chromatography of porcine pancreatic ribonuclease and
RT reinvestigation of the N-terminal amino acid sequence.";
RL FEBS Lett. 31:181-185 (1973).
RN [3]
RP DISULFIDE BONDS.
RX MEDLINE=70104198; PubMed=4904878;
RA Phelan J.J., Hirs C.H.W.;
RT "The primary structure of porcine pancreatic ribonuclease. 3. The
RT disulfide bonds.";
RL J. Biol. Chem. 245:654-661 (1970).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Pancreas.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR PIR: A92071; NRPG.
DR HSP; P00656; 1SRN.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR PRODOM; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84
FT FT 40 95
FT DISULFID 58 110
FT DISULFID 65 72
FT ACT_SITE 12 12
FT ACT_SITE 41 41
FT ACT_SITE 119 119
FT CARBOHYD 21 21
FT CARBOHYD 34 34
FT CARBOHYD 76 76
FT SEQUENCE 124 AA; 13804 MW; 0AC28CDE14111845 CRC64;
KW Query Match 21.6%; Score 129.5; DB 1; Length 124;
Best Local Similarity 30.7%; Pred. No. 4.1e-07;
Matches 35; Conservative 20; Mismatches 42; Indels 17; Gaps 6;
QY 6 FQOKHI-----INTPIICNTLDNNIYVGQCKRVNTFIISATTVAICTGV-INLN 58
DB 8 FORQHMDFDSSSSNSNCVNLMSRR-NWTQCRKPVTNFVHESLADYQAVCSQINVCK 66
QY 59 VLSTTRFQNT-----CTRTSITPRP-CPXSSRTETNYICVKBNQ--YPVHF 103
DB 67 NGQTCNYQSNSTNMTHTDCRQTGSSKVPNCAYKASQEQKHIIIVACEGNPPVPVHF 120
RESULT 10
RNRB BOVIN
ID RNRB BOVIN STANDARD; PRT; 167 AA.
AC P39873;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)

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DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ribonuclease, brain precursor (EC 3.1.1.27.-) (BRB).
GN BRN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92093604; PubMed=1754384;
RA Sasso M.P., Carsana A., Confalone E., Cosi C., Sorrentino S.,
RA Viola M., Palmieri M., Russo E., Furia A.;
RT "Molecular cloning of the gene encoding the bovine brain ribonuclease
RT and its expression in different regions of the brain.";
RL Nucleic Acids Res. 19:6469-6474 (1991).
RN [2]
RP SEQUENCE OF 27-167, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=9214015; PubMed=3243767;
RA Watanabe H., Katoh H., Ishii M., Komoda Y., Sanda A., Takizawa Y.,
RA Ohgi K., Irie M.;
RT "Primary structure of a ribonuclease from bovine brain.";
RL J. Biochem. 104:939-945 (1988).
RN [3]
RP SEQUENCE OF 27-167 FROM N.A.
RX MEDLINE=96139017; PubMed=8587129;
RA Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
RA Vento M.T., Furia A.;
RT "Molecular evolution of genes encoding ribonucleases in ruminant
RT species";
RL J. Mol. Evol. 41:850-858 (1995).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
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CC or send an email to license@sib-sib.ch).
CC EMBL; X59767; CAA42439.1; --
CC EMBL; S81744; AAB36138.1; --
CC PIR; S20066; S20066.
CC HSP; P00656; 2RNS.
CC GlycoSuiteDB; P39873; --
CC InterPro: IPR001427; RNaseA.
CC Pfam; PF00074; RNaseA; 1.
CC PRINTS; PR00794; RIBONUCLEASE.
CC PRODOM; PD000535; RNaseA; 1.
CC SMART; SM00092; RNase_Pc; 1.
CC PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 167 RIBONUCLEASE, BRAIN.
FT ACT_SITE 38 38 BY SIMILARITY.
FT ACT_SITE 67 67 BY SIMILARITY.
FT ACT_SITE 145 145 BY SIMILARITY.
FT DISULFID 52 110 BY SIMILARITY.
FT DISULFID 66 121 BY SIMILARITY.
FT DISULFID 84 136 BY SIMILARITY.
FT DISULFID 91 98 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .).
FT FTID=CAR_000005.
FT CARBOHYD 155 155 O-LINKED.
FT CARBOHYD 159 159 O-LINKED.
FT CONFLICT 155 155 T -> S (IN REF. 2).
SQ SEQUENCE 167 AA; 18450 MW; 681CAAC3CC2FC459 CRC64;
Query Match 21.6%; Score 129.5; DB 1; Length 167;
Best Local Similarity 30.6%; Pred. No. 5.7e-07;

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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [3].  
 RP PARTIAL SEQUENCE.  
 RC TISSUE=Serum;  
 RX MEDLINE=93192291; PubMed=8448182;  
 RA Bond M.D., Strydom D.J., Vallee B.L.;  
 RA "Characterization and sequencing of rabbit, pig and mouse  
 RT angiotensins: discernment of functionally important residues and  
 RT regions.";  
 RL Biochim. Biophys. Acta 1162:177-186 (1993).  
 CC -!- FUNCTION: May function as a tRNA-specific ribonuclease that binds  
 CC to actin on the surface of endothelial cells; once bound,  
 CC angiotensin is endocytosed and translocated to the nucleus, thereby  
 CC promoting the endothelial invasiveness necessary for blood vessel  
 CC formation. Angiotensin induces vascularization of normal and  
 CC malignant tissues. Abolishes protein synthesis by specifically  
 CC hydrolyzing cellular tRNAs.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
 CC  
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 CC  
 CC EMBL; U22516; AAA91366.1; -;  
 CC EMBL; BC055355; AAH5355.1; -;  
 CC PIR; A35932; A35932.  
 CC HSP; P03950; 1A4Y.  
 CC MGD; MG1:88022; Ang.  
 CC InterPro; IPR001427; RNaseA.  
 CC Pfam; PF00074; RNaseA; 1.  
 CC PRINTS; PR00794; RIBONUCLEASE.  
 CC ProDom; PD000535; RNaseA; 1.  
 CC SMART; SM00092; RNase\_Pc; 1.  
 CC PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
 CC KW Hydrolase; Nuclease; Endonuclease; Angiogenesis;  
 CC KW Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.  
 FT SIGNAL 1 24  
 FT CHAIN 25 145  
 FT MOD\_RES 25 25 ANGIOGENIN.  
 FT PYRROLIDONE CARBOXYLIC ACID (BY  
 FT SIMILARITY).  
 FT ACT\_SITE 37 37  
 FT ACT\_SITE 64 64 BY SIMILARITY.  
 FT ACT\_SITE 137 137 BY SIMILARITY.  
 FT DISULFID 50 104 BY SIMILARITY.  
 FT DISULFID 63 115 BY SIMILARITY.  
 FT DISULFID 81 130 BY SIMILARITY.  
 SQ SEQUENCE 145 AA; 16228 MW; 06944260BB764938 CRC64;  
 Query Match 22.8%; Score 136.5; DB 1; Length 145;  
 Best Local Similarity 40.3%; Pred. No. 8.6e-08;  
 Matches 31; Conservative 11; Mismatches 28; Indels 7; Gaps 3;  
 QY 33 CKRVNTFLISSATTVKAICTG-----VINLVNLTSTRFQNTCTRTSITPR-PCPYSSRT 86

Db 63 CKDVNTFHGKSNKAIKANGSPYRENLR-MSKSPFQVITCKTGGSPRPPCOYRASA 121  
 QY 87 ETNYICVKCENQYVHF 103  
 Db 122 GFRHVVIACENGLPVHF 138  
 RESULT 8  
 RNP\_BALAC  
 ID\_RNP\_BALAC STANDARD; PRT; 124 AA.  
 AC PC0673;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).  
 GN RNASE1 OR RNS1.  
 OS Balaenoptera acutorostrata (Minke whale) (lesser rorqual).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;  
 OC Balaenopteridae; Balaenoptera.  
 OX NCBI\_TaxID=9767;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=76277855; PubMed=9628770;  
 RA Emmens M., Welling G.W., Beintema J.J.;  
 RT "The amino acid sequence of pike-whale (lesser-rorqual) pancreatic  
 RT ribonuclease.";  
 RL Biochem. J. 157:317-323 (1976).  
 CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-  
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P  
 CC with 2',3'-cyclic phosphate intermediates.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Pancreas.  
 CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
 CC PIR; A00818; NRWHK.  
 DR HSP; P00656; 1SRN.  
 DR InterPro; IPR001427; RNaseA.  
 DR Pfam; PF00074; RNaseA; 1.  
 DR PRINTS; PR00794; RIBONUCLEASE.  
 DR ProDom; PD000535; RNaseA; 1.  
 DR SMART; SM00092; RNase\_Pc; 1.  
 DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
 DR Hydrolase; Nuclease; Endonuclease; Glycoprotein.  
 FT DISULFID 26 84 BY SIMILARITY.  
 FT DISULFID 40 95 BY SIMILARITY.  
 FT DISULFID 58 110 BY SIMILARITY.  
 FT DISULFID 65 72 BY SIMILARITY.  
 FT ACT\_SITE 12 12 BY SIMILARITY.  
 FT ACT\_SITE 41 41 BY SIMILARITY.  
 FT ACT\_SITE 119 119 BY SIMILARITY.  
 FT CARBOHYD 76 76 N-LINKED (GLCNAC... ) (30%).  
 SQ SEQUENCE 124 AA; 14125 MW; F57475459P697E20 CRC64;  
 Query Match 21.9%; Score 131.5; DB 1; Length 124;  
 Best Local Similarity 32.5%; Pred. No. 2.5e-07;  
 Matches 38; Conservative 17; Mismatches 39; Indels 23; Gaps 7;  
 QY 6 FQQRHII-----NTPIICNTILDNNIYIVGGCKRVNTFISSATTVKAICTGVINLV 59  
 Db 8 FQRQHMDSGNSPCNNENYCNOMMRR-KMTQGRCKPVNTFVHESLEDVKAICS---QKNV 63  
 QY 60 L-----SITRFQNTCTRTSITPR-PCPYSSRTETNYICVKE-NQY-PVHF 103  
 Db 64 LCKNGRTNCTYESNSTMHTDCRQTGSSKYPNCAYKTSQEKHIIIVACEGPNYPVPHF 120  
 RESULT 9  
 RNP\_PIG  
 ID\_RNP\_PIG STANDARD; PRT; 124 AA.  
 AC P00671;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)



```

RT developmentally regulated genes when expressed in NIH 3T3
RL fibroblasts".
RL Mol. Cell. Biol. 17:1503-1512(1997).
CC -!- FUNCTION: Angiogenin induces vascularization of normal and
CC malignant tissues. Abolishes protein synthesis by specifically
CC hydrolyzing cellular tRNAs (By similarity).
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC -----
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CC -----
CC EMBL; U72672; AAC05794.1; -.
CC HSSP; P10152; LAGI.
CC MGD; MGI:1201793; Angl.
CC InterPro; IPR001427; RNaseA.
CC Pfam; PF00074; RNaseA; 1.
CC PRINTS; PR00794; RIBONUCLEASE.
CC ProDom; PD000535; RNaseA; 1.
CC SMART; SM00092; RNase_Pc; 1.
CC PROSITE; PS00127; RNASE_PANCREATIC; 1.
CC KW Hydrolyase; Nuclease; Endonuclease; Angiogenesis;
CC KW Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
FT SIGNAL 1 24
FT CHAIN 25 145
FT MOD_RES 25 25
FT ACT_SITE 37 37
FT ACT_SITE 64 64
FT ACT_SITE 137 137
FT ACT_SITE 104 104
FT DISULFID 50 104
FT DISULFID 63 115
FT DISULFID 81 130
FT SEQUENCE 145 AA; 16696 MW; DE9D3BC92FD1D682C CRC64;
Query Match 25.8%; Score 154.5; DB 1; Length 145;
Best Local Similarity 43.6%; Pred. No. 9.9e-10;
Matches 34; Conservative 12; Mismatches 23; Indels 9; Gaps 4;
QY 33 CKRVNTFIISATTVKAIC-----TGVINLVLTSTFRQNTCTRTSITPR-PCPYSSR 85
Db 63 CKVNTFIHTTKNIKAICGNGRPYGV-NFRI-SNSRFQVTTCTHKGSPRPFCQINAF 120
QY 86 TETNYICVKCENQYPVHF 103
Db 121 KDFRYIVVACEDGWPVHF 138
QY 86 TETNYICVKCENQYPVHF 103
Db 121 KDFRYIVVACEDGWPVHF 138
RESULT 6
ANGR_MOUSE
ID ANGR_MOUSE STANDARD; PRT; 145 AA.
AC Q64438;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiogenin-related protein precursor.
GN ANGRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Liver;
RX MEDLINE=96079109; PubMed=8530072;
RA Brown W.E., Nobile V., Subramanian V., Shapiro R.;
RT "The mouse angiogenin gene family: structures of an angiogenin-related
RL protein gene and two pseudogenes.";
RL Genomics 29:200-206(1995).

```

```

CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U22519; AAA91367.1; -.
CC HSSP; P03950; IA4Y.
CC MGD; MGI:104984; AngRP.
CC InterPro; IPR001427; RNaseA.
CC Pfam; PF00074; RNaseA; 1.
CC PRINTS; PR00794; RIBONUCLEASE.
CC ProDom; PD000535; RNaseA; 1.
CC SMART; SM00092; RNase_Pc; 1.
CC PROSITE; PS00127; RNASE_PANCREATIC; 1.
CC KW Signal; Hydrolase; Nuclease; Endonuclease;
CC KW Pyrrolidone carboxylic acid.
FT SIGNAL 1 24
FT CHAIN 25 145
FT MOD_RES 25 25
FT ACT_SITE 37 37
FT ACT_SITE 64 64
FT ACT_SITE 137 137
FT DISULFID 50 104
FT DISULFID 63 115
FT DISULFID 81 130
FT SEQUENCE 145 AA; 16612 MW; 29A6EB814429C4AD CRC64;
Query Match 24.9%; Score 149.5; DB 1; Length 145;
Best Local Similarity 44.2%; Pred. No. 3.4e-09;
Matches 34; Conservative 9; Mismatches 27; Indels 7; Gaps 3;
QY 33 CKRVNTFIISATTVKAICGV-----INLVLTSTFRQNTCTRTSITPR-PCPYSSRT 86
Db 63 CKVNTFIHTTKNIKAICGKSPYGRNLRI-SKSRFQVTTCTHKGSRPFCRYASK 121
QY 87 TETNYICVKCENQYPVHF 103
Db 122 GFRYIIIGCENGWPVHF 138
RESULT 7
ANGI_MOUSE
ID ANGI_MOUSE STANDARD; PRT; 145 AA.
AC P21570;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
GN ANG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=91025023; PubMed=2222458;
RA Bond M.D., Vallee B.L.;
RT "Isolation and sequencing of mouse angiogenin DNA.";
RL Biochem. Biophys. Res. Commun. 171:988-995(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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CC residues with a 3'-flanking guanine. Hydrolyzes poly(U) and poly(C)
CC as substrates, and prefers the former. The S-lectins in frog eggs
CC may be involved in the fertilization and development of the frog
CC embryo. This lectin agglutinates various animal cells, including
CC normal lymphocytes, erythrocytes, and fibroblasts of animal and
CC human origin. It is cytotoxic against several tumor cells.
CC
CC -1- SUBUNIT: Monomer.
CC
CC -1- SUBCELLULAR LOCATION: Secreted.
CC
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AF039104; AAD10702.1; -.
CC
CC PIR; A27121; A27121.
CC
CC PDB; 1BC4; 28-OCT-98.
CC
CC PDB; 1M07; 21-JAN-03.
CC
CC InterPro; IPR001427; RNaseA.
CC
CC Pfam; PF00074; RNaseA; 1.
CC
CC ProDom; PD000535; RNaseA; 1.
CC
CC SMART; SM00092; RNaseA; 1.
CC
CC PROSITE; PS00127; RNASE PANCREATIC; 1.
CC
CC Hydroxylase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure;
CC
CC KW Signal; Pyrrolidone carboxylic acid.
CC
CC FT CHAIN 1 22 RIBONUCLEASE, OOCVTES.
CC
CC FT MOD_RES 23 133 PYRROLIDONE CARBOXYLIC ACID.
CC
CC FT ACT_SITE 23 23
CC
CC FT ACT_SITE 32 32
CC
CC FT ACT_SITE 57 57
CC
CC FT ACT_SITE 125 125
CC
CC FT DISULFID 41 93
CC
CC FT DISULFID 56 103
CC
CC FT DISULFID 74 118
CC
CC FT DISULFID 115 132
CC
CC FT HELIX 25 32
CC
CC FT HELIX 41 45
CC
CC FT TURN 48 49
CC
CC FT STRAND 59 63
CC
CC FT HELIX 67 73
CC
CC FT TURN 74 74
CC
CC FT STRAND 79 84
CC
CC FT STRAND 90 95
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CC FT STRAND 105 110
CC
CC FT STRAND 114 119
CC
CC FT TURN 120 121
CC
CC FT STRAND 122 129
CC
CC SEQUENCE 133 AA; 14762 MW; A7D62594F7D16F0C CRC64;
CC
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CC Query Match 97.6%; Score 585.5; DB 1; Length 133;
CC Best Local Similarity 97.3%; Pred. No. 3.6e-56;
CC Matches 108; Conservative 2; Mismatches 0; Indels 1; Gaps 1;
CC
CC QY 1 QNWATFOQKHINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNV 59
CC |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
CC
CC DB 23 QNWATFOQKHINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNV 82
CC |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
CC
CC QY 60 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
CC |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
CC
CC DB 83 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 133
CC |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
CC
CC RESULT 2
CC LECs_RANJA STANDARD; PRT; 111 AA.
CC
CC AC P18839;
CC
CC DT 01-NOV-1990 (Rel. 16, Created)
CC
CC DT 01-FEB-1994 (Rel. 28, Last sequence update)
CC
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)

```

```

DE Sialic acid-binding lectin (EC 3.1.1.27.-).
OS Rana japonica (Japanese redbellied frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
OX NCBI_TaxID=8402;
RN [1]
RN SEQUENCE AND DISULFIDE BONDS.
RC TISSUE=Egg;
RC MEDLINE=91035319; PubMed=2229005;
RA Kamiya Y, Oyama F, Oyama R., Sakakibara F., Nitta K., Kawachi H.,
RA Takayanagi Y., Tani K.,
RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
RT eggs."
RL J. Biochem. 108:139-143(1990).
CC -1- FUNCTION: The S-lectins in frog eggs may be involved in the
CC fertilization and development of the frog embryo. This lectin
CC preferentially agglutinates a large variety of tumor cells, but it
CC does not agglutinate non-transformed cells and erythrocytes.
CC
CC -1- SUBUNIT: Monomer.
CC
CC -1- SUBCELLULAR LOCATION: Secreted.
CC
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC
CC PIR; JX0120; JX0120.
CC
CC HSP; P11916; IBC4.
CC
CC InterPro; IPR001427; RNaseA.
CC
CC Pfam; PF00074; RNaseA; 1.
CC
CC ProDom; PD000535; RNaseA; 1.
CC
CC SMART; SM00092; RNaseA; 1.
CC
CC PROSITE; PS00127; RNASE PANCREATIC; 1.
CC
CC Hydroxylase; Nuclease; Endonuclease; Sialic acid; Lectin;
CC
CC KW Pyrrolidone carboxylic acid.
CC
CC FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
CC
CC FT ACT_SITE 10 10 BY SIMILARITY.
CC
CC FT ACT_SITE 35 35 BY SIMILARITY.
CC
CC FT ACT_SITE 104 104 BY SIMILARITY.
CC
CC FT DISULFID 19 72
CC
CC FT DISULFID 34 82
CC
CC FT DISULFID 52 97
CC
CC FT DISULFID 94 111
CC
CC SEQUENCE 111 AA; 12326 MW; FDEBDF3834ED679 CRC64;
CC
CC
CC Query Match 75.2%; Score 451; DB 1; Length 111;
CC Best Local Similarity 77.5%; Pred. No. 9e-42;
CC Matches 86; Conservative 8; Mismatches 15; Indels 2; Gaps 2;
CC
CC QY 1 QNWATFOQKHINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVKAICTGV-INLN 58
CC |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
CC
CC DB 1 QNWATFOQKHINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVKAICTGV-INLN 60
CC |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
CC
CC QY 59 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRGC 109
CC |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
CC
CC DB 61 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRGC 111
CC |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
CC
CC RESULT 3
CC RNPL_RANCA STANDARD; PRT; 111 AA.
CC
CC ID RNPL_RANCA STANDARD; PRT; 111 AA.
CC
CC AC P14626;
CC
CC DT 01-APR-1990 (Rel. 14, Created)
CC
CC DT 01-FEB-1994 (Rel. 28, Last sequence update)
CC
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC
CC DE Ribonuclease, liver (EC 3.1.1.27.5).
CC
CC OS Rana catesbeiana (Bull frog).
CC
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
CC
CC OX NCBI_TaxID=8400;
CC
CC RN [1]
CC
CC RN SEQUENCE.
CC
CC RC TISSUE=Liver;
CC
CC RX MEDLINE=90130374; PubMed=2613682;
CC
CC RA Nitta K., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
CC
CC RA Okazaki T., Ohgi K., Irie M.;
CC
CC RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
CC liver."

```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:30:40 ; Search time 5.55659 Seconds  
(without alignments)  
1030.796 Million cell updates/sec

Title: US-09-961-400-19

Perfect score: 600

Sequence: 1 QNWFQKHIIINTPIICNT.....ICVKENQYPVHFAGIGRCP 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	585.5	97.6	133	1	RNPO_RANCA
2	451	75.2	111	1	LECS_RANJA
3	370	61.7	111	1	RNPL_RANCA
4	273.5	45.6	104	1	RN30_RANPI
5	154.5	25.8	145	1	ANG3_MOUSE
6	149.5	24.9	145	1	ANGR_MOUSE
7	136.5	22.8	145	1	ANGI_MOUSE
8	131.5	21.9	124	1	RNP_BALAC
9	129.5	21.6	124	1	RNP_PIG
10	129.5	21.6	167	1	RNBR_BOVIN
11	127.5	21.2	119	1	RNP_IGUIG
12	124.5	20.8	151	1	RNBR_CAPCA
13	123.5	20.6	123	1	ANG2_BOVIN
14	123.5	20.6	141	1	RNBR_GIRCA
15	123.5	20.6	151	1	RNBR_AXIPR
16	123	20.5	146	1	ANGI_MIOXA
17	123	20.5	146	1	ANGI_SAISC
18	120	20.0	146	1	ANGI_CERAE
19	120	20.0	147	1	ANGI_PONPY
20	119.5	19.9	143	1	RNBR_SHEEP
21	119	19.8	122	1	RNP_MACRU
22	118.5	19.8	123	1	ANGI_PIG
23	118.5	19.8	124	1	RNP_ANTAM
24	118	19.7	146	1	ANGI_AOTTR
25	117	19.5	146	1	ANGI_SAGOE
26	116.5	19.4	128	1	RNP_MYOCO
27	116.5	19.4	149	1	RNP_MOUSE
28	115	19.2	146	1	ANGI_MACMU
29	114.5	19.1	128	1	RNBP_CAVPO
30	114	19.0	148	1	ANGI_BOVIN
31	113.5	18.9	124	1	RNP_CANDR
32	113.5	18.9	128	1	RNP_HORSE
33	113	18.8	147	1	ANGI_HUMAN

34 113 18.8 147 1 ANGI\_PANTR  
35 112.5 18.8 119 1 RNS4\_BOVIN  
36 112.5 18.8 128 1 RNP\_FROGU  
37 109.5 18.2 124 1 RNP\_RANTA  
38 109.5 18.2 146 1 ANGI\_PAPHA  
39 109.5 18.2 148 1 RNS4\_MOUSE  
40 109 18.2 125 1 ANGI\_RABIT  
41 108.5 18.1 124 1 RNP\_CAPCA  
42 108.5 18.1 124 1 RNP\_GIRCA  
43 108.5 18.1 130 1 RNP\_CRILO  
44 107.5 17.9 124 1 RNP\_BUBBU  
45 107.5 17.9 148 1 RNP\_PERLE

Q8wme8 pan troglod  
P15467 bos taurus  
P04059 proechimys  
P00666 rangifer ta  
Q8wn64 papio hamad  
Q97jhl mus musculus  
P31347 oryctolagus  
P00664 capreolus c  
P00662 giraffa cam  
P24717 cricetus  
P00657 bubalus bub  
Q9wnv5 peromyscus

#### ALIGNMENTS

RESULT 1  
RNPO\_RANCA STANDARD; PRT; 133 AA.  
AC P11916; Q9PWR7;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ribonuclease, oocytes precursor (EC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SBL-C).  
DE binding lectin)  
GN RCR.  
OS Rana catesbeiana (Bull frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
OX NCBI\_TaxID=8400;  
[1]  
SEQUENCE FROM N.A.  
RP TISSUE=Liver;  
RC MEDLINE=98165825; PubMed=9497370;  
RA Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;  
RT "The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease. Tissue distribution, cloning, purification, cytotoxicity, and active residues for RNase activity.";  
RL J. Biol. Chem. 273:6395-6401(1998).  
[2]  
SEQUENCE OF 23-133.  
RP TISSUE=Egg;  
RC MEDLINE=87299649; PubMed=3304421;  
RA Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawachi H., Takayanagi G., Hakomori S.;  
RT "Amino acid sequence of sialic acid binding lectin from frog (Rana catesbeiana) eggs.";  
RL Biochemistry 26:2189-2194(1987).  
[3]  
CHARACTERIZATION, AND SEQUENCE OF 81-101.  
RC MEDLINE=92220613; PubMed=1373237;  
RA Liao Y.-D.;  
RT "A pyrimidine-guanine sequence-specific ribonuclease from Rana catesbeiana (bullfrog) oocytes.";  
RL Nucleic Acids Res. 20:1371-1377(1992).  
[4]  
CHARACTERIZATION.  
RC TISSUE=Egg;  
RA Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawachi H., Takayanagi Y., Hakomori S., Titani K.;  
RT "Ribonuclease activity of sialic acid-binding lectin from Rana catesbeiana eggs.";  
RL Glycobiology 3:37-45(1993).  
[5]  
STRUCTURE BY NMR OF 23-133.  
RC MEDLINE=98437383; PubMed=9761686;  
RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;  
RT "The solution structure of a cytotoxic ribonuclease from the oocytes of Rana catesbeiana (bullfrog).";  
RL J. Mol. Biol. 283:231-244(1998).  
CC -!- FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine

Search completed: May 7, 2004, 21:54:56  
Job time : 10.9813 secs



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Db 7 FQHQHMDTEHSTASSNYCNLMKAR-DMTSGRCKPLNTFIHPEKSVVDVACHQENVTCK 65
QY 52 TGVINLVLTTRFQNLCTRTSTITPRP-CPYSSRTETNYICVKENQY-PVHF 103
Db 66 NGRNTNC-YKSNRLSITNCRTQGTASKYPNCQYETSINLQKIIVACEGQYVPVHF 118

RESULT 11
A43825
angiogenin - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S29834; A43825
R:Bond, M.D.; Strydom, D.J.; Vallsee, B.L.
Biochim. Biophys. Acta 1162, 177-186, 1993
A:Title: Characterization and sequencing of rabbit, pig and mouse angiogenins: disclerme
A:Reference number: S29833; MUID:93192291; PMID:8448162
A:Accession: S29834
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-123 <SON>
A>Note: this sequence was submitted to the Protein Sequence Database, December 1992
C:Superfamily: pancreatic ribonuclease

Query Match 19.8%; Score 118.5; DB 1; Length 123;
Best Local Similarity 39.5%; Pred. No. 9.3e-05;
Matches 30; Conservative 6; Mismatches 35; Indels 5; Gaps 2;

QY 33 CKRVNTFIISATTVKAICTG-----VINLVLTTRFQNLCTRTSTITPR-PCYSSRTE 87
Db 39 CKEVNTFHGRNDKAIKNDKNGEPYNNFRSKSPFOITCKHKGGSNRPFCGYRATAG 98

QY 88 TNYICVKENQYVPVHF 103
Db 99 PRTIACVACENGLPVHF 114

RESULT 12
NRPRI
pancreatic ribonuclease (EC 3.1.27.5) - pronghorn (tentative sequence)
N:Alternate names: RNase 1; RNase A
C:Species: Antilocapra americana (pronghorn)
C>Date: 28-Feb-1991 #sequence_revision 28-Feb-1991 #text_change 31-Mar-2000
C:Accession: A00813
R:Beintema, J.J.; Gastra, W.; Munniksma, J.
J. Mol. Evol. 13, 305-316, 1979
A:Title: Primary structure of pronghorn pancreatic ribonuclease: close relationship betw
A:Reference number: A00813; MUID:80075014; PMID:513141
A:Accession: A00813
A:Molecule type: protein
A:Residues: 1-124 <BE>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12,41,119/Active site: His, Lys, His #status predicted
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F:34/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 19.8%; Score 118.5; DB 1; Length 124;
Best Local Similarity 29.9%; Pred. No. 9.3e-05;
Matches 35; Conservative 19; Mismatches 44; Indels 19; Gaps 7;

QY 4 ANFOQKHINTPI-----ICNTILDNNIYVGGQCKRVNTFIISATTVKAICT----- 52
Db 6 AKFEROHIDNSPSSVSSSNYCNQMKSR-NLTQGRCKPNTFVHESLADVQAVCSKNVA 64

QY 53 ---GVINLVLTTRFQNLCTRTSTITPRP-CPYSSRTETNYICVKE-NQY-PVHF 103
Db 65 CKNGQTCNC-YQSYSTYSITDCRTGSSKYPNCAYKTQAKKHLIVACEGPNYPVPHY 120

RESULT 13
NRCU
pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)
N:Alternate names: RNase 1; RNase A
C:Species: Myocastor coypus (nutria, coypu)
C>Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C:Accession: A00822
R:van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
A:Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic
A:Reference number: A90612; MUID:77065676; PMID:999896
A:Accession: A00822
A:Molecule type: protein
A:Residues: 1-128 <VAN>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12,41,119/Active site: His, Lys, His #status predicted
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 19.4%; Score 116.5; DB 1; Length 128;
Best Local Similarity 30.8%; Pred. No. 0.00015;
Matches 36; Conservative 16; Mismatches 42; Indels 23; Gaps 7;

QY 6 FQOKHI-----INTPIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVINLV 59
Db 8 FERQHDMSRGSPSTPNYCNEMKSR-NMTQGRCKPNTFVHEPLADVQAVC---FQKNV 63

QY 60 L-----STTRFQNLCTRTSTITPRP-CPYSSRTETNYICVKE-NQY-PVHF 103
Db 64 LCKNGQTCNCYSNSNMHITDCRVTSNDSYDPCSVYRTSQEEKSIIVACEGPNYPVPHF 120

RESULT 14
NRMS
pancreatic ribonuclease (EC 3.1.27.5) precursor - mouse
N:Alternate names: RNase 1; RNase A
C:Species: Mus musculus (house mouse)
C>Date: 30-Nov-1980 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999
C:Accession: A34090; S22598; A00830
R:Schueller, C.; Nijssen, H.M.J.; Kok, R.; Beintema, J.J.
Mol. Biol. Evol. 7, 29-44, 1990
A:Title: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of mouse
A:Reference number: A34090; MUID:90136034; PMID:2299980
A:Accession: A34090
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-149 <SCH>
A:Cross-references: GB:M27814; NID:g200762; PIDN:AAA40060.1; PID:g200763
R:Samuelson, L.C.; Wiebauer, K.; Howard, G.; Schmid, R.M.; Koeplin, D.; Meisler, M.H.
Nucleic Acids Res. 19, 6935-6941, 1991
A:Title: Isolation of the murine ribonuclease gene Rib-1: structure and tissue specific
A:Reference number: S22598; MUID:92107684; PMID:1840677
A:Accession: S22598
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-149 <SAM>
A:Cross-references: EMBL:X60103; NID:g53981; PIDN:CAA42697.1; PID:g53982
R:Lenstra, J.A.; Beintema, J.J.
Eur. J. Biochem. 98, 399-408, 1979
A:Title: The amino acid sequence of mouse pancreatic ribonuclease.
A:Reference number: A00830; MUID:80024269; PMID:556267
A:Accession: A00830
A:Molecule type: protein
A:Residues: 26-149 <LEN>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-149/Product: pancreatic ribonuclease #status experimental <MAT>
F:37,66,144/Active site: His, Lys, His #status predicted
F:51-109,65-120,83-135,90-97/Disulfide bonds: #status predicted
F:62,87/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.4%; Score 116.5; DB 1; Length 149;
Best Local Similarity 29.9%; Pred. No. 0.00018;
Matches 35; Conservative 17; Mismatches 42; Indels 23; Gaps 7;
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```

;;Molecule type: protein
;;Residues: 27-154, 'S', 156-166 <WAT>
;;Experimental source: brain
;;Superfamily: pancreatic ribonuclease
;;Keywords: glycoprotein; hydrolase
;;52-110, 66-121, 84-136, 91-98/Disulfide bonds: #status predicted
;;88/Binding site: carboxylate (Asn) (covalent) #status experimental
;;85/Binding site: carboxylate (Thr) (covalent) #status experimental
;;159/Binding site: carboxylate (Ser) (covalent) #status experimental

```

C:Superfamily: pancreatic ribonuclease  
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
F:12.41.119/Active site: His, Lys, His #status predicted  
F:21.34.76/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:26-84,40-55,58-110,65-72/Disulfide bonds: #status experimental

```

;;Molecule type: protein
;;Residues: 27-154, 'S', 156-166 <WAT>
;;Experimental source: brain
;;Superfamily: pancreatic ribonuclease
;;Keywords: glycoprotein; hydrolase
;;52-110, 66-121, 84-136, 91-98/Disulfide bonds: #status predicted
;;88/Binding site: carboxylate (Asn) (covalent) #status experimental
;;85/Binding site: carboxylate (Thr) (covalent) #status experimental
;;159/Binding site: carboxylate (Ser) (covalent) #status experimental

```

[illegible]



```

QY      1 QNWATFOOKHIINTP-IICNTILDNNIYIVGGCKRWNTFISSATTVKAICTGV-INLN 58
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DBD     1 QNWAKEFKHPTNSINCMNTIMKSIYIVGGCKERNFTFISSATTVKAICSGASTNRN 60
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||

QY      59 VLSTTRFQLNCTRTSITPRPCPYSSRTEITNYICVKENQYPVHFAGIGRC 109
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DBD     61 VLSTTRFQLNCTRSATAPRPCPNYSRTETNVICVKCNRLPVHPFAGIGRC 111
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||

RESULT 3
X0085
pancreatic ribonuclease (EC 3.1.27.5) - bullfrog
C:Species: Rana catesbeiana (bullfrog)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
E:Accession: JX0085
J:Author: Katayama, N.; Okabe, Y.; Iwana, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Ohguchi, J. Biochem. 106, 729-735, 1989
A:Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
A:Reference number: JX0085; MUID:90130374; PMID:2613682
A:Accession: JX0085
A:Molecule type: Protein
A:Residues: 1-111 <NIT>
C:Superfamily: pancreatic ribonuclease
C:Keywords: hydrolase; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:P10_35,104/Active site: His, Lys, His #status predicted
F:P19-72,34-82,52-97,94-111/Disulfide bonds: #status predicted

Query Match 61.7%; Score 370; DB 2; Length 111;
Best Local Similarity 64.9%; Pred. No. 1.le-29;
Matches 72; Conservative 10; Mismatches 27; Indels 2; Gaps 2;

QY      1 QNWATFOOKHIINTPII-CNTILDNNIYIVGGCKRWNTFISSATTVKAICTGV-I-NLN 58
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DBD     1 QNWAKEFKHIRSTSIDCNTIMDKAIYIVGGCKERNFTFISSDNVKAICSGVSPDRK 60
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||

QY      59 VLSTTRFQLNCTRTSITPRPCPYSSRTEITNYICVKENQYPVHFAGIGRC 109
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DBD     61 FLSTTSFKTNTCTRDSTITPRPCPHSPDNNKI CVKCEKOLPVHFVGIGRC 111
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||

```

```

RESULT 4
A39035 ribonuclease-related anti-tumor protein - northern leopard frog (fragment)
C;Species: Rana pipiens (northern leopard frog)
C;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
C;Accession: A39035
R;Ardelet, W.; Mikulski, S.M.; Shogen, K.
J. Biol. Chem. 266, 245-251, 1991
A;Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl
A;Reference number: A39035; MUID:91093131; PMID:1995896
A;Accession: A39035
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-104 <ARD>
C;Superfamily: pancreatic ribonuclease

Query Match          45.1%; Score 270.5; DB 2; Length 104;
Best Local Similarity 47.7%; Pred. No. 7.1e-20;
Matches 53; Conservative 17; Mismatches 32; Indels 9; Gaps 4;

Qy      1 QNWATFOOKHAIINT-PIICNTILDNNYIVYGQCKRVNTHFISSATTVKAICTGVI-NLN 58
        :|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db      1 EDWLTFQKHITNTRDVCDDIMSTNLF---HCKDKNTFYISREPVPVKALCKGIISK 56
        :|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:

Qy      59 VLSTTRFQINCTRTSIITREPCPYSSRTETNYI CVKENOYVHFAGIGRC 109
        :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
        57 VLTWSEFFVISDC--NVTSRPCKYKI KYSTNKFKVTCENAPVFHVGVGSC 104

```

RESULT 5  
A35932  
angiogenin precursor - mouse

V;Alternate names: angiogenesis factor  
V;Contains: ribonuclease (EC 3.1.1.27.-)  
C;Species: Mus musculus (house mouse)  
C;Date: 09-Nov-1990 #sequence\_revision 09-Nov-1990 #text\_change 18-Jun-1999  
C;Accession: A35932

R;Bond, M.D.; Vallee, B.L.  
Biochem. Biophys. Res. Commun. 171, 988-995, 1990  
A;Title: Isolation and sequencing of mouse angiogenin DNA.  
A;Reference number: A35932; MUID:91025023; PMID:2222458  
A;Accession: A35932  
A;Status: not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-145 <BON>  
A;Cross-references: GB:U22516; NID:g726325; PIDN:AAA91366.1; PID:g726326  
C;Genetics:  
A;Introns: #status absent  
C;Function:  
C;Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues  
C;Superfamily: pancreatic ribonuclease  
C;Keywords: angiogenesis; hydrolase; nucleic acid degradation; pyroglutamic acid  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-145/Product: angiogenin #status predicted <WAT>  
F;25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted  
F;37,64,137/Active site: His, Lys, His #status predicted  
F;50-104,63-115,81-130/Disulfide bonds: #status predicted

Query Match 22.8%; Score 136.5; DB 1; Length 145;  
Best Local Similarity 40.3%; Pred. No. 1.8e-06;  
Matches 31; Conservative 11; Mismatches 28; Indels 7; Gaps 3;

QY 33 CKRVNTFTLISSATTVAICTG-----VINLVLSITRFPOLNCTRTSITPR-PCPVSSRT 86  
|| ||||| : : ||||| : : ||||| : : ||||| : : ||||| : :  
Db 63 CKDVTFTIHNKSNIAICANGSPYRENL-RMSKPFQVTTCKTGSGRPFCQYRAS 121  
|| : : ||||| : : ||||| : : ||||| : : ||||| : : ||||| : :  
QY 87 ETNYICVKCNQYPVHF 103  
: : : |||||  
Db 122 GFRHVVIACENGLPVPVF 138  
: : : |||||

RESULT 6  
NRWHK  
pancreatic ribonuclease (EC 3.1.1.27.5) - minke whale  
N;Alternate names: RNase 1; RNase A  
C;Species: Balaeoptera acutorostrata (minke whale, lesser rorqual)  
C;Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 03-Jun-1994  
C;Accession: A00818  
R;Emmens, M.; Welling, G.W.; Beintema, J.J.  
Biochem. J. 157, 317-323, 1976  
A;Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease.  
A;Reference number: A00818; MUID:76277855; PMID:962870  
A;Accession: A00818  
A;Molecule type: protein  
A;Residues: 1-124 <EMM>  
C;Superfamily: pancreatic ribonuclease  
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
F;12,41,119/Active site: His, Lys, His #status predicted  
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted  
F;76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 21.9%; Score 131.5; DB 1; Length 124;  
Best Local Similarity 32.5%; Pred. No. 4.8e-06;  
Matches 38; Conservative 17; Mismatches 39; Indels 23; Gaps 7;

QY 6 FQQKHII-----NTPPICHTILDNNIYIVGGCKRVNTFTLISSATTVAICTGVINLV 59  
: : : ||||| : : ||||| : : ||||| : : ||||| : : ||||| : :  
Db 8 FQRQHMDSGNSPGNPNCQMWR-R-KMTQGRCKPNTFVHESLEDVKAVCS---QKNV 63  
: : : ||||| : : ||||| : : ||||| : : ||||| : : ||||| : :  
QY 60 L-----STTRFPLNCTRTSITPR-CPYSSRTETNYICVKE-NQY-EVHF 103  
: : : ||||| : : ||||| : : ||||| : : ||||| : : ||||| : :  
Db 64 LCKNGRNCHVESNTMHITDCRQTGSSKYFNCAKYTSQEKHHIVACEGNFYVPVHF 120  
: : : ||||| : : ||||| : : ||||| : : ||||| : : ||||| : :

RESULT 7

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:38:36 ; Search time 9.98129 Seconds  
(without alignments)  
1060.090 Million cell updates/sec

Title: US-09-961-400-19  
Perfect score: 600  
Sequence: 1 QNWATFOQKHINTPIICNT.....TCVKCENQYPVHFAGIGRCP 110  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues  
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78.\*  
1: Pir1.\*  
2: Pir2.\*  
3: Pir3.\*  
4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	582.5	97.1	111	2 A27121	ribonuclease-relat
2	451	75.2	111	1 JX0120	ribonuclease-relat
3	370	61.7	111	2 JX0085	pancreatic ribonuc
4	270.5	45.1	104	2 A39035	ribonuclease-relat
5	136.5	22.8	145	1 A35932	angiogenin precurs
6	131.5	21.9	124	1 NRWHK	pancreatic ribonuc
7	129.5	21.6	124	1 NRPHK	pancreatic ribonuc
8	129.5	21.6	167	2 S20066	pancreatic-type ri
9	127.5	21.2	119	2 S41111	pancreatic ribonuc
10	119	19.8	122	1 NRKGR	pancreatic ribonuc
11	118.5	19.8	123	1 A43825	angiogenin - pig
12	118.5	19.8	124	1 NRPRH	pancreatic ribonuc
13	116.5	18.4	128	1 NRCU	pancreatic ribonuc
14	116.5	19.4	149	1 NRCMS	pancreatic ribonuc
15	114.5	19.0	125	1 NRGPB	pancreatic ribonuc
16	114	19.1	128	1 A32474	angiogenin [valida
17	113.5	18.9	124	1 NRCM	pancreatic ribonuc
18	113.5	18.9	124	1 NRCMM	pancreatic ribonuc
19	113.5	18.9	124	1 NRCMB	pancreatic ribonuc
20	113.5	18.9	128	1 NRHOG	pancreatic ribonuc
21	113	18.8	147	1 NRHUG	angiogenin precurs
22	112.5	18.8	128	1 NRKS	pancreatic ribonuc
23	110.5	18.4	124	2 S08549	pancreatic ribonuc
24	109.5	18.2	124	1 NRDEN	pancreatic ribonuc
25	109	18.2	125	1 B43825	angiogenin - rabbi
26	108.5	18.1	124	1 NRGF	pancreatic ribonuc
27	108.5	18.1	124	1 NRDEO	pancreatic ribonuc
28	108.5	18.1	130	2 S22808	pancreatic ribonuc
29	107.5	17.9	124	1 NRWB	pancreatic ribonuc

## ALIGNMENTS

## RESULT 1

A27121  
ribonuclease-related sialic acid-binding lectin - bullfrog  
C:Species: Rana catesbeiana (bullfrog)  
C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 30-Jun-1993  
C:Accession: A27121  
R;Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawauchi, H.; Takayanagi, J. Biochem. 108, 139-143, 1990  
A:Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)  
A:Reference number: A27121; MUID:87299649; PMID:3304421  
A:Accession: A27121  
A:Molecule type: protein  
A:Residues: 1-111 <TIT>  
C:Superfamily: pancreatic ribonuclease  
C:Keywords: lectin

Query Match 97.1%; Score 582.5; DB 2; Length 111;  
Best Local Similarity 96.4%; Pred. No. 1e-50;  
Matches 107; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 QNWATFOQKHINTPII-CNTILDNNIYVGGCKRVNTPIISSATTVKAICTGVINLVN 59  
DB 1 ENWATFOQKHINTPIICNTINDNNIYVGGCKRVNTPIISSATTVKAICTGVINMV 60  
QY 60 LSTTRFQLNTCTTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110  
DB 61 LSTTRFQLNTCTTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

## RESULT 2

JX0120  
ribonuclease-related sialic acid-binding lectin - Japanese frog  
C:Species: Rana japonica (Japanese frog)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: JX0120  
R;Kamaya, I.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawauchi, H.; Takayanagi, J. Biochem. 108, 139-143, 1990  
A:Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.  
A:Reference number: JX0120; MUID:91035319; PMID:2229005  
A:Accession: JX0120  
A:Molecule type: protein  
A:Residues: 1-111 <KAW>  
A:Experimental source: egg  
C:Superfamily: pancreatic ribonuclease  
C:Keywords: lectin; pyroglutamic acid  
P.1/Modified site: pyroglutamic acid (Gln) #status experimental  
F.19-72,34-82,52-97,94-111/Disulfide bonds: #status experimental

Query Match 75.2%; Score 451; DB 1; Length 111;  
Best Local Similarity 77.5%; Pred. No. 1e-37;  
Matches 86; Conservative 8; Mismatches 15; Indels 2; Gaps 2;





Sat May 8 17:57:17 2004

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Rana pipiens
; DEVELOPMENTAL STAGE: Embryo
US-08-283-971-1
Query Match 45.1%; Score 270.5; DB 1; Length 104;
Best Local Similarity 47.7%; Pred. No. 6.5e-24;
Matches 53; Conservative 17; Mismatches 32; Indels 9; Gaps 4;
QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKAITGVINLN 58
Db 1 EDWLTQKKHITNRDVCNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASKN 56
QY 59 VLSTTRPQNTCTRTSITPRPCPSYSTRFTNYICVKCENQYVHFAGIGRC 109
Db 57 VLATSEFYLSDC---NVTSPCKYKUKKSTNKFVCVCENQAPVHFVGVGSC 104
RESULT 13
US-07-921-619-1
; Sequence 1, Application US/07921619
; Patent No. 5595734
; GENERAL INFORMATION:
; APPLICANT: Ardelt Ph.D. Wojciech J.
; APPLICANT: Mikulski, Stanislaw M.
; TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark H. Jay, P.C.
; STREET: P.O. Box 020083, General Post Office
; CITY: Brooklyn
; STATE: New York
; COUNTRY: USA
; ZIP: 11202-0002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/921,619
; FILING DATE: 19920728
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/178,118
; FILING DATE: 06-APR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/436,141
; FILING DATE: 13-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Jay, Mark H.
; REGISTRATION NUMBER: 27507
; REFERENCE/DOCKET NUMBER: 5005 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 718-625-0399
; TELEFAX: 718-625-0399
; TELEX: No. 5595734 Applicable
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
```

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; ORIGINAL SOURCE:
; ORGANISM: Rana pipiens
; DEVELOPMENTAL STAGE: Embryo
US-07-921-619-1
Query Match 45.1%; Score 270.5; DB 1; Length 104;
Best Local Similarity 47.7%; Pred. No. 6.5e-24;
Matches 53; Conservative 17; Mismatches 32; Indels 9; Gaps 4;
QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKAITGVINLN 58
Db 1 EDWLTQKKHITNRDVCNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASKN 56
QY 59 VLSTTRPQNTCTRTSITPRPCPSYSTRFTNYICVKCENQYVHFAGIGRC 109
Db 57 VLATSEFYLSDC---NVTSPCKYKUKKSTNKFVCVCENQAPVHFVGVGSC 104
RESULT 14
US-08-467-955-1
; Sequence 1, Application US/08467955
; Patent No. 5728805
; GENERAL INFORMATION:
; APPLICANT: Ardelt Ph.D. Wojciech J.
; TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark H. Jay, P.A.
; STREET: P.O. Box E
; CITY: Short Hills
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07078-0383
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,955
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/178,118
; FILING DATE: 06-APR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/436,141
; FILING DATE: 13-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,332
; FILING DATE: 03-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,970
; FILING DATE: 01-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jay, Mark H.
; REGISTRATION NUMBER: 27507
; REFERENCE/DOCKET NUMBER: 5007 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-912-9066
; TELEFAX: 201-912-0442
; TELEX: No. 5728805 Applicable
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 63:
; LENGTH: 129 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-63

Query Match 45.6%; Score 273.5; DB 3; Length 129;
Best Local Similarity 48.6%; Pred. No. 3.8e-24;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOOKHIINT-PIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVI-NLN 58
Db 26 QDWLTFOKKHITNTRDVDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 81
QY 59 VLSTTRFQMLNCTRTSTITPRPCPYSSRTETNYICVKENQYVHFAGIGRC 109
Db 82 VLTTSFYLSDC---NVTSPCKYKUKKSTNKFVCVCENQAPVHFVGVGSC 129

RESULT 11
US-08-875-811-43
; Sequence 43, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
```

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; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 379 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-43

Query Match 45.6%; Score 273.5; DB 3; Length 379;
Best Local Similarity 48.6%; Pred. No. 1.4e-23;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOOKHIINT-PIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVI-NLN 58
Db 26 QDWLTFOKKHITNTRDVDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 81
QY 59 VLSTTRFQMLNCTRTSTITPRPCPYSSRTETNYICVKENQYVHFAGIGRC 109
Db 82 VLTTSFYLSDC---NVTSPCKYKUKKSTNKFVCVCENQAPVHFVGVGSC 129

RESULT 12
US-08-283-971-1
; Sequence 1, Application US/08283971
; Patent No. 5529775
; GENERAL INFORMATION:
; APPLICANT: Ardelt Ph.D, Wojciech J.
; APPLICANT: Mikulski, Stanislaw M.
; TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark H. Jay, P.C.
; STREET: P.O. Box 020083, General Post Office
; CITY: Brooklyn
; STATE: New York
; COUNTRY: USA
; ZIP: 11202-0002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/283,971
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/921,180
; FILING DATE: 30-JUL-1992
; APPLICATION NUMBER: US 07/178,118
; FILING DATE: 06-APR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/436,141
; FILING DATE: 13-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Jay, Mark H.
; REGISTRATION NUMBER: 27507
; REFERENCE/DOCKET NUMBER: 5006 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 718-625-0399
; TELEFAX: 718-625-0399
; TELEX: No. 5529775 Applicable
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
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APPLICANT: Ardelet, Wojciech
TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which
TITLE OF INVENTION: Allows Production by Recombinant Methods
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,429
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/626,288
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ran, David B.
REGISTRATION NUMBER: 38,589
REFERENCE/DOCKET NUMBER: 15280-267
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-095-429-1

Query Match 45.6%; Score 273.5; DB 4; Length 104
Best Local Similarity 48.6%; Pred. No. 2.9e-24;
Matches 54; Conservative 16; Mismatches 32; Indels 59

QY      1 QNWATFOQKHINT-PITCNTILDNNIIVGQCKRVNTFIILSSATTYKAI
Db       |::|||:|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|
        1 QDWLTFQKKHHTNRDVCDCNIMSNLF---HCXDKNTFIYSRREPVKAI
QY      59 VLSTFRFLQNTCTRTSITPRPCPYSSRTEINVCNKENQYVPHFAGICRC
Db       ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
        57 VLTTSFYLSDC---NVTSRPCKYKLKSTNKFCTVCENQAQPVHFVGVSQC

RESULT 10
; Sequence 63, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluis
; APPLICANT: Wlodaver, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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97      59 VLSTTRPQLNCTRTSITPRPCPYSSRTEINYICVKENQYPVHFAIGRC 109
98      ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|||
99      57 VLTTFSEFLSDC---NVTCRPCKYKLLKSKTNKFCVTCENQAPVHFVGSGC 104
100
101 RESULT 8
102 US-08-626-288-1
103 : Sequence 1, Application US/08626288
104 : Patent No. 6649392
105 : GENERAL INFORMATION:
106 : APPLICANT: Youle, Richard
107 : APPLICANT: Vasandani, Veena
108 : APPLICANT: Wu, Yon-Neng
109 : APPLICANT: Boix, Ester
110 : APPLICANT: Ardelet, Wojciech
111 TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which
112 TITLE OF INVENTION: Allows Production by Recombinant Methods
113 NUMBER OF SEQUENCES: 3
114 CORRESPONDENCE ADDRESS:
115 ADDRESSEE: Townsend and Townsend and Crew
116 STREET: One Market Plaza, Steuart Street Tower
117 CITY: San Francisco
118 STATE: California
119 COUNTRY: USA
120 ZIP: 94105-1492
121 COMPUTER READABLE FORM:
122 MEDIUM TYPE: Floppy disk
123 COMPUTER: IBM PC compatible
124 OPERATING SYSTEM: PC-DOS/MS-DOS
125 SOFTWARE: Patent In Release #1.0, Version #1.30
126 CURRENT APPLICATION DATA:
127 APPLICATION NUMBER: US/08/626,288
128 FILING DATE: NO. 6649392 yet assigned
129 CLASSIFICATION: 530
130 ATTORNEY/AGENT INFORMATION:
131 NAME: Ran, David B.
132 REGISTRATION NUMBER: 38,589
133 REFERENCE/DOCKET NUMBER: 15280-267
134 TELECOMMUNICATION INFORMATION:
135 TELEPHONE: (415) 543-9600
136 TELEFAX: (415) 543-5043
137 INFORMATION FOR SEQ ID NO: 1:
138 SEQUENCE CHARACTERISTICS:
139 LENGTH: 104 amino acids
140 TYPE: amino acid
141 STRANDEDNESS:
142 TOPOLOGY: linear
143 MOLECULE TYPE: protein
144 US-08-626-288-1
145
146 Query Match 45.6%; Score 273.5; DB 4; Length 104;
147 Best Local Similarity 48.6%; Pred.No. 2.9e-24; Indels 9; Gaps 4;
148 Matches 54; Conservative 16; Mismatches 32;
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150 QY 1 QNWATFOOKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISATTVKAICTGVI-NLN 58
151 ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|||
152 Db 1 QDWLTFQKKHITNRDVCNINSLNF---HCKDKNTFYSRPEVPVKAICKGILASKN 56
153
154 QY 59 VLSTTRPQLNCTRTSITPRPCPYSSRTEINYICVKENQYPVHFAIGRC 109
155 ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|||
156 Db 57 VLTTFSEFLSDC---NVTSRPCYKYLKSKTNKFCVTCENQAPVHFVGSGC 104
157
158 RESULT 9
159 US-09-095-429-1
160 : Sequence 1, Application US/09095429
161 : Patent No. 6649393
162 : GENERAL INFORMATION:
163 : APPLICANT: Youle, Richard
164 : APPLICANT: Vasandani, Veena
165 : APPLICANT: Wu, Yon-Neng
166 : APPLICANT: Boix, Ester

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DEVELOPMENTAL STAGE: oocyte  
US-08-467-955-2

Query Match 46.8%; Score 280.5; DB 1; Length 104;  
Best Local Similarity 48.6%; Pred. No. 4.5e-25;  
Matches 54; Conservation 17.7%.

Statistics	Conservative	Mismatches	Indels	Gaps
Matches	34	17	31	9
Mismatches	3	1	1	1
Indels	0	0	0	0
Gaps	0	0	0	0

Qy 1 QNWATFQQKHIINT-PIICNTILDNNIYVGQCXRVTFLISSATTVAICTGVI-NLN 58  
::|||::||::||::||::||::||::||::||::||::||::||::||::||  
Db 1 EDWLTQKKHVTNTRDVDGNINMSTLNF---HCCKDFTFYSRPEPVAICKGIASKN 56

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Qy 59 VLSTTRFQLNCTRTSITPRCPYSSRTETNYICVKENQYPVHFAGIRC 109
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Db 57 VLTTSSEFYLSDC---NVTSRCPKYKLXKSTWKFVCVTENQAIPVFHVGVRC 104
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RESULT 4
US-09-394-268-1
/ Sequence 1, Application US/09394268
/ Patent No. 6175003
/ GENERAL INFORMATION:
/ APPLICANT: Saxena, Shailendra K
/ TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF
/ TITLE OF INVENTION: MAKING THEM
/ FILE REFERENCE: 5013
/ CURRENT APPLICATION NUMBER: US/09/394,268
/ CURRENT FILING DATE: 1999-09-10
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 104
/ TYPE: PRT
/ ORGANISM: Rana pipiens
US-09-394-268-1

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Query Match 45.6%; Score 273.5; DB 3; Length 104;  
Best Local Similarity 48.6%; Pred. No. 2.9e-24;  
Matches 54: Conservative 15; Moderate 15; Divergent 24

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1 QNWATFOQKHINT-PIICNTILDNNIYVGGCKRVNFISSATTVKACITGV-I-NLN 58				
1 QDWLTFQKHINTRDVDCDNIWSTNLF----HCKDKNTFIYSRPPFVKACIGIATSKN 56				

[illegible]

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RESULT 5
US-09-394-268-2
; Sequence 2, Application US/09394268
; Patent No. 6175003
; GENERAL INFORMATION:
; APPLICANT: Saxena, Shailendra K
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF
; TITLE OF INVENTION: MAKING THEM
; FILE REFERENCE: 5013
; CURRENT APPLICATION NUMBER: US/09/394,268
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SEQ ID NO:1 with Leu at position 23 and Cys at
; OTHER INFORMATION: position 72
US-09-394-268-2

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Query Match 45.6%; Score 273.5; DB 3; Length 104;  
Best Local Similarity 49.5%; Pred. No. 2.9e-24;  
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

[illegible]

## RESULT 6

US-09-687-748-1  
; Sequence 1, Application US/09687748  
; Patent No. 6423515

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; GENERAL INFORMATION:
; APPLICANT: Saxena, Shailendra K
; TITLE OF INVENTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
; FILE REFERENCE: 5013 US 01
; CURRENT APPLICATION NUMBER: US/09/687,748
; CURRENT FILING DATE: 2000-10-14
; PRIOR APPLICATION NUMBER: 09/394,268
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-687-748-1

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Query Match 45.6%; Score 273.5; DB 4; Length 104;  
Best Local Similarity 48.6%; Pred. No. 2.9e-24;  
Matches 54. Conservative 100.0%  
100.0%  
100.0%

	Conservative	Indels	Mismatches	Gaps
1 QNWATFQQRHINT-PIICNTILDNNIYIVGQCKRVNTFISSATTVKAICTGVI-NUN 58		:		
1 QDMLTQKKHINTRVDCNIMSTNLF-----HCKDKNTFIVSRPEPKACKGIIASKN 56		:		

59 VLSTRFQLNTCTSTITPPCPYSSRTETNYICVKCENQVPVHFAGIGRC 109  
|||:|||:|||||:|||||:|||||:|||||:|||||:|||||:  
57 VLTTSERYLSDC---NVTSPCKYLKSKNKFCVTCENQAPVHFCVGSC 104

RESIST, T 7

US-09-687-748-2  
Sequence 2, Application US/09687748  
Patent No. 6423515

GENERAL INFORMATION:  
 APPLICANT: Saxena, Shaileendra K  
 TITLE OF INVENTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES  
 FILE REFERENCE: 5013 US 01  
 CURRENT APPLICATION NUMBER: US/09/687,748  
 CURRENT FILING DATE: 2000-10-14  
 PRIOR APPLICATION NUMBER: 09/394,268  
 PRIOR FILING DATE: 1999-09-10  
 NUMBER OF SEQ ID NOS: 8  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 2  
 LENGTH: 104  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: SEQ ID NO:1 with Leu at position 23 and Cys at position 72  
 OTHER INFORMATION: position 72  
 S-09-687-748-2

Query Match	45.6%	Score 273.5	DB 4	Length 104
Best Local Similarity	49.5%	Pred. No. 2.9e-24		
Matches	55	Conservative	15	Mismatches 32
			Indels	9
			Gaps	4

1 QNWATFOQKHINT-PIICNTILDNIIYVGGQCKRVNTPFIISATTVKACITGV-I-NLN 58  
! : !  
1 QDWLTFQKKHTNRDVEDCNILSTNLF-----HCKDKNTFYIRSPERPVAKICIGTISK 56



us-09-961-400-19.ra1

Sat May 8 17:57:17 2004

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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..111
; OTHER INFORMATION: /note= "Frog Lectin from Rana
; OTHER INFORMATION: catesbeiana"
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Query Match 97.1%; Score 582.5; DB 2; Length 111;
Best Local Similarity 96.4%; Pred. No. 6.4e-60;
Matches 107; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 QNWATFOQKHINTPII-ONTILDNNIYVGGQCKRVNTFISSATTVAICTGVNLNV 59
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Db 1 ENWATFOQKHINTPIINCNTIMDNNIYVGGQCKRVNTFISSATTVAICTGVNLNV 60

QY 60 LSTTRFQNLCTCTSTTPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
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Db 61 LSTTRFQNLCTCTSTTPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 3
US-08-467-955-2
; Sequence 2, Application US/08467955
; Patent No. 5728805
; GENERAL INFORMATION:
; APPLICANT: Ardelit Ph.D. Wojciech J.
; TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark H. Jay, P.A.
; STREET: P.O. Box E
; CITY: Short Hills
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07078-0383
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,955
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/178,118
; FILING DATE: 06-APR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/436,141
; FILING DATE: 13-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,332
; FILING DATE: 03-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,970
; FILING DATE: 01-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jay, Mark H.
; REGISTRATION NUMBER: 27507
; REFERENCE/DOCKET NUMBER: 5007 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-912-9066
; TELEFAX: 201-912-0442
; TELEX: No. 5728805 Applicable
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Rana pipiens
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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..111
; OTHER INFORMATION: /note= "Frog Lectin from Rana
; OTHER INFORMATION: catesbeiana"
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US-08-891-848-12
Query Match 97.1%; Score 582.5; DB 2; Length 111;
Best Local Similarity 96.4%; Pred. No. 6.4e-60;
Matches 107; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 QNWATFOQKHINTPII-ONTILDNNIYVGGQCKRVNTFISSATTVAICTGVNLNV 59
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 ENWATFOQKHINTPIINCNTIMDNNIYVGGQCKRVNTFISSATTVAICTGVNLNV 60

QY 60 LSTTRFQNLCTCTSTTPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 LSTTRFQNLCTCTSTTPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 2
US-08-875-811-8
; Sequence 8, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..111
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:28:45 ; Search time 12.7596 Seconds  
(without alignments)  
445.066 Million cell updates/sec

Title: US-09-961-400-19  
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Sequence: 1 QNATFQKHINTPIICNT.....ICVKENQYVHFAGIGRCP 110

Scoring table: BLOSUM62  
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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/2/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B COMB.pep.\*  
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6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	582.5	97.1	111	2	US-08-891-848-12
2	582.5	97.1	111	3	US-08-875-811-8
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4	273.5	45.6	104	3	US-09-394-268-1
5	273.5	45.6	104	3	US-09-394-268-2
6	273.5	45.6	104	4	US-09-687-748-1
7	273.5	45.6	104	4	US-09-687-748-2
8	273.5	45.6	104	4	US-08-626-288-1
9	273.5	45.6	104	4	US-09-095-429-1
10	273.5	45.6	129	3	US-08-875-811-63
11	273.5	45.6	379	3	US-08-283-971-1
12	270.5	45.1	104	1	US-08-875-811-43
13	270.5	45.1	104	1	US-07-921-619-1
14	270.5	45.1	104	1	US-08-467-955-1
15	270.5	45.1	104	2	US-08-891-848-13
16	270.5	45.1	104	4	US-08-626-288-2
17	270.5	45.1	104	4	US-09-095-429-2
18	270.5	45.1	105	3	US-08-875-811-39
19	270.5	45.1	355	3	US-08-875-811-41
20	270.5	45.1	358	3	US-08-875-811-51
21	268.5	44.8	104	3	US-08-875-811-1
22	268.5	44.8	104	4	US-09-071-672-1
23	268.5	44.8	104	4	US-08-986-119-1
24	268.5	44.8	106	3	US-08-875-811-28
25	268.5	44.8	107	3	US-08-875-811-30
26	268.5	44.8	112	3	US-08-875-811-32
27	268.5	44.8	251	3	US-08-875-811-59

## ALIGNMENTS

RESULT 1  
US-08-891-848-12  
Sequence 12, Application US/08891848  
Patent No. 5955073  
GENERAL INFORMATION:  
APPLICANT: Rybak, Susanna M.  
APPLICANT: Youle, Richard J.  
APPLICANT: Newton, Dianne L.  
APPLICANT: Nicholls, Peter J.  
TITLE OF INVENTION: Selective RNase Cytotoxic Reagents  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM: disk  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/891,848  
FILING DATE: No. 5955073 yet assigned  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/125,462  
FILING DATE: 22-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/014,082  
FILING DATE: 04-FEB-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/779,195  
FILING DATE: 22-OCT-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/510,696  
FILING DATE: 20-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 015280-110310US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 111 amino acids  
TYPE: amino acid

Sequence 61, Appl  
Sequence 49, Appl  
Sequence 57, Appl  
Sequence 64, Appl  
Sequence 55, Appl  
Sequence 26, Appl  
Sequence 24, Appl  
Sequence 45, Appl  
Sequence 53, Appl  
Sequence 20, Appl  
Sequence 22, Appl  
Sequence 3, Appl  
Sequence 47, Appl  
Sequence 2, Appl  
Sequence 1, Appl  
Sequence 4, Appl  
Sequence 2, Appl  
Sequence 3, Appl

28 268.5 44.8 254 3 US-08-875-811-61  
29 268.5 44.8 355 3 US-08-875-811-49  
30 268.5 44.8 355 3 US-08-875-811-57  
31 268.5 44.8 355 3 US-08-875-811-64  
32 268.5 44.8 366 3 US-08-875-811-55  
33 263.5 43.9 105 3 US-08-875-811-24  
34 263.5 43.9 105 3 US-08-875-811-26  
35 259.5 43.2 358 3 US-08-875-811-45  
36 259.5 43.2 365 3 US-08-875-811-53  
37 245.5 40.9 107 3 US-08-875-811-20  
38 235.5 39.2 111 3 US-08-875-811-22  
39 232 38.7 114 3 US-09-223-118-3  
40 223.5 37.2 360 3 US-08-875-811-47  
41 223 37.2 114 3 US-09-223-118-2  
42 222 37.0 114 3 US-09-223-118-1  
43 221 36.8 114 3 US-09-223-118-4  
44 202 33.7 83 3 US-08-875-811-2  
45 202 33.7 83 4 US-09-071-672-3

OS Rana pipiens.  
XX WO9738112-A1.  
PN  
XX 16-OCT-1997.  
PD  
XX 04-APR-1997; 97WO-US005675.  
PF  
XX 04-APR-1996; 96US-00625288.  
PR  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA  
XX Youle RJ, Vasandani VM, Wu Y, Boix E, Ardelt W;  
PI  
XX WPI; 1997-512725/47.  
DR  
XX  
XX Recombinant Onc protein with glutamine residue at position 1 - useful as  
PT antitumour and antiviral agent, also as cell culture selection agent.  
PT  
XX Claim 1; Page 28; 35pp; English.  
PS  
XX This sequence represents a recombinant Onc protein comprising a 104 amino  
CC acid sequence having Gln at position 1. Onc, a ribonuclease from Rana  
CC pipiens oocytes, is known as an antitumour agent (e.g. for treating  
CC pancreatic cancer) and inhibitor of human immunodeficiency virus type-1  
CC replication. It can be used therapeutically or as a cell-culture  
CC selection agent, e.g. to identify gene therapy compositions able to  
CC inhibit tumour growth  
XX  
SQ Sequence 104 AA;  
Query Match 45.6%; Score 273.5; DB 2; Length 104;  
Best Local Similarity 48.6%; Pred. No. 5.5e-23;  
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;  
QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVI-NLN 58  
Db 1 QDWLTFQKHITNTDRDVCNLLSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKN 56  
QY 59 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109  
Db 57 VLTTSEFYLSDC---NVTSRPCYKYLKSTNKFVCVCENQAPVHFVGVGSC 104  
RESULT 15  
AAB31667  
ID AAB31667 standard; protein; 104 AA.  
XX  
AC AAB31667;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Amino acid sequence of a modified frog ribonuclease protein.  
XX  
KW Frog; ribonuclease; ranpirnase; RNase.  
XX  
OS Synthetic.  
OS Rana pipiens.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 23  
FT /note= "wild type Met changed to Leu"  
FT Misc-difference 72  
FT /note= "wild type Ser changed to Cys"  
XX  
XX US6175003-B1.  
PN  
XX  
PD 16-JAN-2001.  
XX  
XX 10-SEP-1999; 99US-00394268.  
PF  
XX 10-SEP-1999; 99US-00394268.  
PR  
XX

PA (ALFA-) ALFACELL CORP.  
XX  
PI Saxena SK;  
XX  
DR WPI; 2001-167808/17.  
XX  
PT New nucleic acids encoding a ribonuclease (K Nase), useful for the precise  
PT targeting of K Nase to a predetermined cell receptor.  
XX  
XX Claim 2; Col 5-6; 7pp; English.  
XX  
XX The present sequence represents a modified frog ribonuclease protein  
CC (ranpirnase) (RNase). The synthetic ribonuclease comprises a cysteine  
CC which facilitates the chemical linking of a targeting molecule by the  
CC single reactive sulphydryl group. The specification describes a method  
CC for the production of ranpirnase using DNA technology instead of  
CC processing biological material. The re-engineering of the protein  
CC molecule allows easier attachment to a targeting molecule thereby making  
CC it possible for the ribonuclease to be delivered to a particular cell  
CC receptor where it might be most effective  
XX  
SQ Sequence 104 AA;  
Query Match 45.6%; Score 273.5; DB 4; Length 104;  
Best Local Similarity 49.5%; Pred. No. 5.5e-23;  
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;  
QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVI-NLN 58  
Db 1 QDWLTFQKHITNTDRDVCNLLSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKN 56  
QY 59 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109  
Db 57 VLTTSEFYLSDC---NVTSRPCYKYLKSTNKFVCVCENQAPVHFVGVGSC 104  
Search completed: May 7, 2004, 21:38:29  
Job time : 47.9224 secs

KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;  
 KW Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;  
 KW recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;  
 XX autoimmune disease.

OS Rana pipiens.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Misc-difference 1  
 FT /note= "Met not found in wild type RaPLR1"

PN WO9950398-A2.

PD 07-OCT-1999.

PF 26-MAR-1999; 99WO-US006641.

PR 27-MAR-1998; 98US-0079751P.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PI Rybak SM, Newton DL;

DR WPI; 1999-610847/52.

DR N-PSDB; AAZ08126.

XX New recombinant ribonucleases, used for killing target cells, e.g. for

FT treating cancers, viral infections or autoimmune diseases.

XX Claim 34; Page 57; 71pp; English.

XX The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1)

CC protein with Met at position 1. Carboxy terminal end of recombinant

CC RaPLR1 has a covalently bound ligand binding moiety, which can be a LL2

CC antibody directed against CD22 on cancerous B cells or human chorionic

CC gonadotropin (hCG) effective against Kaposi's sarcoma cells. Recombinant

CC ribonucleases can be expressed in bacteria without an N-terminal

CC methionine due to the presence of a signal peptide that is cleaved by

CC bacteria. The soluble expression of ribonuclease allows the proteins to

CC be fused in-frame with ligand binding moieties to form cytotoxic fusion

CC proteins. They can be used for treatment of cancer and autoimmune

CC diseases

XX Sequence 105 AA;

SQ Query Match 46.2%; Score 277.5; DB 2; Length 105;

Best Local Similarity 48.6%; Pred. No. 2e-23;

Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGQCKRVNTFISSATTVKATCGVI-NLN 58

Db 2 QDWLTFQKHLNTRDVCNIMSTNLF---HCKDKNTFYSRPEPVKAIKGIATSKN 57

QY 59 VLSTTRFQNLCTRTSITPRPCPSYSTRTNYICVKENQYVPHFAGIGRC 109

Db 58 VLTTSEFVLSDC---NVTSRPCKYKLLKSTNTFCVTCENQAPVPHFVGVC 105

RESULT 13

AAV28879

ID AAV28879 standard; protein; 127 AA.

XX AC AAV28879;

XX 25-JAN-2000 (first entry)

XX Rana pipiens Clone Salb ribonuclease.

XX Rana pipiens ribonuclease Clone Salb; RaPLR1; covalently bound; RNase;

XX LL2 antibody; ligand binding moiety; CD22; cancerous B cell; onconase;

XX Kaposi's Sarcoma; human chorionic gonadotropin; hCG; cancer;

XX recombinant ribonuclease; frog; signal peptide; cytotoxic fusion protein;

KW autoimmune disease.  
 XX Rana pipiens.  
 OS Rana pipiens.  
 FH Key Location/Qualifiers  
 FT Peptide 1..23  
 FT /label= Signal\_peptide  
 FT /note= "Putative"  
 FT 24..127  
 FT Protein  
 FT /label= Rana\_pipiens\_Clone\_Salb\_ribonuclease

PN WO9950398-A2.

PD 07-OCT-1999.

PF 26-MAR-1999; 99WO-US006641.

PR 27-MAR-1998; 98US-0079751P.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Rybak SM, Newton DL;

DR WPI; 1999-610847/52.

DR N-PSDB; AAZ08136.

XX New recombinant ribonucleases, used for killing target cells, e.g. for

FT treating cancers, viral infections or autoimmune diseases.

XX Disclosure; Page 69; 71pp; English.

XX The present sequence is a Rana pipiens Clone Salb ribonuclease (RaPLR1).

CC It is encoded by Clone Salb cDNA obtained from Rana pipiens liver mRNA

CC library. It exhibits differences with Onconase (RTM) at amino acid

CC residues 11, 20, 85 and 103. Carboxy terminal end of RaPLR1 has a

CC covalently bound ligand binding moiety, which can be a LL2 antibody

CC directed against CD22 on cancerous B cells or human chorionic

CC gonadotropin (hCG) effective against Kaposi's Sarcoma cells. Recombinant

CC ribonucleases can be expressed in bacteria without an N-terminal

CC methionine due to the presence of a signal peptide that is cleaved by

CC bacteria. The soluble expression of ribonuclease allows the proteins to

CC be fused in-frame with ligand binding moieties to form cytotoxic fusion

CC proteins. They can be used for treatment of cancer and autoimmune

CC diseases

XX Sequence 127 AA;

SQ Query Match 46.2%; Score 277.5; DB 2; Length 127;

Best Local Similarity 48.6%; Pred. No. 2.5e-23;

Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGQCKRVNTFISSATTVKATCGVI-NLN 58

Db 24 QDWLTFQKHLNTRDVCNIMSTNLF---HCKDKNTFYSRPEPVKAIKGIATSKN 79

QY 59 VLSTTRFQNLCTRTSITPRPCPSYSTRTNYICVKENQYVPHFAGIGRC 109

Db 80 VLTTSEFVLSDC---NVTSRPCKYKLLKSTNTFCVTCENQAPVPHFVGVC 127

RESULT 14

AAW30301

ID AAW30301 standard; protein; 104 AA.

XX AC AAW30301;

XX 09-JUN-1998 (first entry)

XX Recombinant onc protein.

XX Onc; oncanase; ribonuclease; frog; antitumor; pancreatic cancer;

XX human immunodeficiency virus type-1; HIV1; replication.

ID AAY28869 standard; protein; 105 AA.  
 XX  
 AC AAY28869;  
 XX  
 DT 25-JAN-2000 (first entry)  
 XX  
 DE Recombinant Met(-1) RaPLR1 Met23Leu-(His)6 protein.  
 XX  
 KW Recombinant Met(-1) Rana pipiens ribonuclease Met23Leu-(His)6; RaPLR1;  
 XX CD22; covalently bound; LL2 antibody; ligand binding moiety; RNase;  
 KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotropin; hCG;  
 KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;  
 KW cancer; frog; autoimmune disease.  
 XX  
 OS Rana pipiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 XX  
 FT Misc-difference 1 /note= "Met not found in wild type RaPLR1"  
 FT  
 FT Misc-difference 1 /note= "(His)6 histidine tag attached to N-terminal Met"  
 FT  
 FT Misc-difference 24 /note= "Wild type Met replaced with Leu"  
 FT  
 XX WO9950398-A2.  
 XX  
 XX 07-OCT-1999.  
 XX  
 XX 26-MAR-1999; 99WO-US006641.  
 XX  
 XX 27-MAR-1998; 98US-0079751P.  
 XX  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 XX Rybak SM, Newton DL;  
 XX  
 XX WPI; 1999-610847/52.  
 DR  
 DR N-PSDB; AAZ08127.  
 XX  
 XX New recombinant ribonucleases, used for killing target cells, e.g. for  
 XX treating cancers, viral infections or autoimmune diseases.  
 XX  
 XX Claim 4; Page 59; 71pp; English.  
 XX  
 XX The present sequence is a recombinant Rana pipiens ribonuclease protein  
 XX (RaPLR1) with Met at position 1 attached to (His)6 tag and Met24Leu.  
 XX Carboxy terminal end of recombinant RaPLR1 has a covalently bound ligand  
 XX binding moiety, which can be a LL2 antibody directed against CD22 on  
 XX cancerous B cells or human chorionic gonadotropin (hCG) effective  
 XX against Kaposi's sarcoma cells. Recombinant ribonucleases can be  
 XX expressed in bacteria without an N-terminal methionine due to the  
 XX presence of a signal peptide that is cleaved by bacteria. The soluble  
 XX expression of ribonuclease allows the proteins to be fused in-frame with  
 XX ligand binding moieties to form cytotoxic fusion proteins. They can be  
 XX used for treatment of cancer and autoimmune diseases  
 XX  
 XX Sequence 105 AA;  
 XX  
 XX Query Match 46.6%; Score 279.5; DB 2; Length 105;  
 XX Best Local Similarity 49.5%; Pred. No. 1.2e-23;  
 XX Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;  
 QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NLN 58  
 DB 2 QDWLTFQKHLTNTDVCNNILTNLF---HCKDKNTFIYSRPEPVKAICKGIASKN 57  
 QY 59 VLSTTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRC 109  
 DB 58 VLTTSEFYLSDC---NVTSRPCYKYLKKSNTFCVTCENQAPVHFVGVGHC 105  
 RESULT 11

AAY28865  
 ID AAY28865 standard; protein; 104 AA.  
 XX  
 AC AAY28865;  
 XX  
 DT 25-JAN-2000 (first entry)  
 XX  
 DE Rana pipiens liver ribonuclease (RaPLR1).  
 XX  
 KW Rana pipiens liver ribonuclease; RaPLR1; covalently bound; LL2 antibody;  
 XX ligand binding moiety; CD22; cancerous B cell; Kaposi's Sarcoma; frog;  
 KW human chorionic gonadotropin; hCG; recombinant ribonuclease; RNase;  
 KW signal peptide; cytotoxic fusion protein; cancer; autoimmune disease.  
 XX  
 OS Rana pipiens.  
 XX  
 PN WO9950398-A2.  
 XX  
 XX 07-OCT-1999.  
 XX  
 XX 26-MAR-1999; 99WO-US006641.  
 XX  
 XX 27-MAR-1998; 98US-0079751P.  
 XX  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 XX Rybak SM, Newton DL;  
 XX  
 XX WPI; 1999-610847/52.  
 DR  
 DR N-PSDB; AAZ08124.  
 XX  
 XX New recombinant ribonucleases, used for killing target cells, e.g. for  
 XX treating cancers, viral infections or autoimmune diseases.  
 XX  
 XX Claim 1; Page 55; 71pp; English.  
 XX  
 XX The present sequence is Rana pipiens liver ribonuclease (RaPLR1) protein.  
 XX Carboxy terminal end of RaPLR1 has a covalently bound ligand binding  
 XX moiety, which can be a LL2 antibody directed against CD22 on cancerous B  
 XX cells or human chorionic gonadotropin (hCG) effective against Kaposi's  
 XX Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria  
 XX without an N-terminal methionine due to the presence of a signal peptide  
 XX that is cleaved by bacteria. The soluble expression of ribonuclease  
 XX allows the proteins to be fused in-frame with ligand binding moieties to  
 XX form cytotoxic fusion proteins. They can be used for treatment of cancer  
 XX and autoimmune diseases  
 XX  
 XX Sequence 104 AA;  
 XX  
 XX Query Match 46.2%; Score 277.5; DB 2; Length 104;  
 XX Best Local Similarity 48.6%; Pred. No. 1.9e-23;  
 XX Matches 54; Conservative 16; Mismatches 33; Indels 9; Gaps 4;  
 QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NLN 58  
 DB 1 QDWLTFQKHLTNTDVCNNILTNLF---HCKDKNTFIYSRPEPVKAICKGIASKN 56  
 QY 59 VLSTTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRC 109  
 DB 57 VLTTSEFYLSDC---NVTSRPCYKYLKKSNTFCVTCENQAPVHFVGVGHC 104  
 RESULT 12  
 AAY28867  
 ID AAY28867 standard; protein; 105 AA.  
 XX  
 AC AAY28867;  
 XX  
 DT 25-JAN-2000 (first entry)  
 XX  
 DE Recombinant Met(-1) RaPLR1.  
 XX  
 KW Recombinant Met(-1) Rana pipiens ribonuclease; RaPLR1; CD22; RNase;

```

CC (Rana catesbeiana) lectin used to describe the method of the invention
XX
SQ Sequence 111 AA;

Query Match          97.1%; Score 582.5; DB 2; Length 111;
Best Local Similarity 96.4%; Pred. No. 6.5e-58;
Matches 107; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 QNWATFOQKHINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 59
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DQ 1 ENWATFOQKHINTPIINCNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60
QY 60 LSTTRFQNTCTRTSITPRPCPSYSTRTETNYICVKCENQYVHFAGIGRCP 110
DQ :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DQ 61 LSTTRFQNTCTRTSITPRPCPSYSTRTETNYICVKCENQYVHFAGIGRCP 111

RESULT 8
AAW06544
ID ID AAW06544 standard; protein; 104 AA.
XX
AC AAW06544;
XX
DT 22-AUG-1997 (first entry)
XX
DE Antitumour protein from Rana pipiens oocytes.
XX
KW Tumour; chemotherapy; radiotherapy; frog.
XX
OS Rana pipiens.
XX
PN WO9639428-A1.
XX
PD 12-DEC-1996.
XX
PF 03-JUN-1996; 96WO-US008304.
XX
PR 06-JUN-1995; 95US-00467955.
XX
PA (ALFA-) ALFACELL CORP.
XX
PI Ardelt WJ;
XX
PS WPI; 1997-043063/04.
XX
PT Antitumour proteins from Rana pipiens oocyte(s) - have fewer
PT disadvantages than chemotherapy, surgery and radiotherapy.
XX
PS Claim 8; Page 28; 45pp; English.
XX
CC The present sequence is a specifically claimed example of an antitumour
CC protein from the generic protein in AAW18224, with the molecular weight
CC 12000. This is one of two preferred proteins (the other in AAW06543) that
CC have been isolated from Rana pipiens oocytes. Both proteins have a
CC blocked amino terminal group and are essentially free of carbohydrates.
CC The proteins are used to treat tumours. Use of the peptides has fewer
CC disadvantages than chemotherapy, radiotherapy and surgery in the
CC treatment of tumours
XX
SQ Sequence 104 AA;

Query Match          46.8%; Score 280.5; DB 2; Length 104;
Best Local Similarity 48.6%; Pred. No. 8.8e-24;
Matches 54; Conservative 17; Mismatches 31; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NLN 58
DQ :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DQ 1 EDWLTFOQKHINTRDVDNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 56
QY 59 VLSTTRFQNTCTRTSITPRPCPSYSTRTETNYICVKCENQYVHFAGIGRGC 109
DQ :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DQ 57 VLTTFSEFYLSDC---NVTSRPCQKYLKXSTNKFCTVCENQAPVHFVGVGRC 104

```

```

RESULT 9
AAW28866
ID ID AAY28866 standard; protein; 104 AA.
XX
AC AAY28866;
XX
DT 25-JAN-2000 (first entry)
XX
DE Recombinant RaPLR1 Met23Leu amino acid sequence.
XX
KW Recombinant Rana pipiens ribonuclease; RaPLR1 Met23Leu; covalently bound;
KW LL2 antibody; ligand binding moiety; CD22; cancerous B cell; RNase;
KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
KW recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
KW autoimmune disease.
XX
OS Rana pipiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 23 /note= "Wild type Met replaced with Leu"
XX
PN WO9950398-A2.
XX
PD 07-OCT-1999.
XX
PF 26-MAR-1999; 99WO-US006641.
XX
PR 27-MAR-1998; 98US-0079751P.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rybak SM, Newton DL;
XX
DR WPI; 1999-610847/52.
DR N-PSDB; AAZ08125.
XX
PT New recombinant ribonucleases, used for killing target cells, e.g. for
PT treating cancers, viral infections or autoimmune diseases.
XX
PS Claim 34; Page 56; 71pp; English.
XX
CC The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1)
CC protein with Met23Leu. Carboxy terminal end of recombinant RaPLR1 has a
CC covalently bound ligand binding moiety, which can be a LL2 antibody
CC directed against CD22 on cancerous B cells or human chorionic
CC gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant
CC ribonucleases can be expressed in bacteria without an N-terminal
CC methionine due to the presence of a signal peptide that is cleaved by
CC bacteria. The soluble expression of ribonuclease allows the proteins to
CC be fused in-frame with ligand binding moieties to form cytotoxic fusion
CC proteins. They can be used for treatment of cancer and autoimmune
CC diseases
XX
SQ Sequence 104 AA;

Query Match          46.6%; Score 279.5; DB 2; Length 104;
Best Local Similarity 49.5%; Pred. No. 1.1e-23;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NLN 58
DQ :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DQ 1 QDWLTFOQKHINTRDVDNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 56
QY 59 VLSTTRFQNTCTRTSITPRPCPSYSTRTETNYICVKCENQYVHFAGIGRGC 109
DQ :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DQ 57 VLTTFSEFYLSDC---NVTSRPCQKYLKXSTNKFCTVCENQAPVHFVGVGHC 104

RESULT 10
AAW28869

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us-09-961-400-19.rag

Sat May 8 17:57:17 2004

SQ Sequence 110 AA;

Query Match 98.5%; Score 591; DB 2; Length 110;  
Best Local Similarity 98.2%; Pred. No. 7.1e-59;  
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWATFQKHINTPIICNTILDNNIYVGGQCKRVNTFIISATTVKATCTGVINLVLS 61  
DB 2 NWATFQKHINTPIICNTILDNNIYVGGQCKRVNTFIISATTVKATCTGVINLVLS 61

QY 62 TTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYVHPFAGIGRCP 110  
DB 62 TTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYVHPFAGIGRCP 110

RESULT 6  
AAY28878  
ID AAY28878 standard; protein; 111 AA.  
XX AC AAY28878;  
XX DT 25-JAN-2000 (first entry)  
XX DE Recombinant Met (-1) RaCOR1 Gln1Ser amino acid sequence.  
XX KW Recombinant Met (-1) Rana catesbeiana oocyte ribonuclease Gln1Ser; RaCOR1;  
KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;  
KW Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;  
KW recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;  
KW CD22; RNase; autoimmune disease.  
XX OS Rana catesbeiana.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"  
FT Misc-difference 2 /note= "Wild type Gln replaced with Ser"  
XX WO9950398-A2.  
XX PD 07-OCT-1999.  
XX PF 26-MAR-1999; 99WO-US006641.  
XX PF 27-MAR-1998; 98US-0079751P.  
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Rybak SM, Newton DL;  
XX PS WPI; 1999-610847/52.  
XX DR N-PSDB; AA208135.  
XX PT New recombinant ribonucleases, used for killing target cells, e.g. for  
XX treating cancers, viral infections or autoimmune diseases.  
XX PS Claim 22; Page 68; 71pp; English.  
XX CC The present sequence is a recombinant Rana catesbeiana ribonuclease  
XX (RaCOR1) protein with Met at position 1 and Gln2Ser. Carboxy terminal end  
XX of recombinant RaCOR1 has a covalently bound ligand binding moiety, which  
XX can be a LL2 antibody directed against CD22 on cancerous B cells or human  
XX chorionic gonadotropin (hCG) effective against Kaposi's sarcoma cells.  
XX Recombinant ribonucleases can be expressed in bacteria without an N-  
XX terminal methionine due to the presence of a signal peptide that is  
XX cleaved by bacteria. The soluble expression of ribonuclease allows the  
XX proteins to be fused in-frame with ligand binding moieties to form  
XX cytotoxic fusion proteins. They can be used for treatment of cancer and  
XX autoimmune diseases  
XX SQ Sequence 111 AA;

Query Match 98.5%; Score 591; DB 2; Length 111;  
Best Local Similarity 98.2%; Pred. No. 7.1e-59;  
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWATFQKHINTPIICNTILDNNIYVGGQCKRVNTFIISATTVKATCTGVINLVLS 61  
DB 3 NWATFQKHINTPIICNTILDNNIYVGGQCKRVNTFIISATTVKATCTGVINLVLS 62

QY 62 TTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYVHPFAGIGRCP 110  
DB 63 TTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYVHPFAGIGRCP 111

RESULT 7  
AAY33321  
ID AAY33321 standard; protein; 111 AA.  
XX AC AAY33321;  
XX DT 29-NOV-1999 (first entry)  
XX DE Frog lectin protein fragment.  
XX KW Cytotoxic; RNase; ribonuclease; pancreatic; antibody; light chain;  
KW heavy chain; cell surface marker; treatment; tumor; viral infection;  
KW parasite infection; immune dysfunctional cell; autoimmune disease;  
KW contraceptive; cell separation; transplantation; bone marrow ablation;  
KW leukemia cell; T-cell; graft-versus-host disease; bullfrog; lectin.  
XX OS Rana catesbeiana.  
XX OS US955073-A.  
XX PD 21-SEP-1999.  
XX PF 09-JUL-1997; 97US-00891848.  
XX PF 20-APR-1990; 90US-00510696.  
XX PR 22-OCT-1991; 91US-0079195.  
XX PR 04-FEB-1993; 93US-00014082.  
XX PR 22-SEP-1993; 93US-00125462.  
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Rybak SM, Newton DL, Nicholls PJ, Youle RJ;  
XX DR WPI; 1999-560488/47.  
XX PT Recombinantly fused pancreatic RNase-targeting proteins useful for  
XX treating tumors, infections, immune or autoimmune disorders and as a  
XX contraceptive.  
XX PS Example 3; Fig 19; 47pp; English.  
XX CC This invention describes a novel nucleic acid construct comprising  
XX sequences encoding functional pancreatic RNase and a second protein  
XX (preferably the light and heavy chains of an antibody) which binds a  
XX specific cell surface marker on a target cell and functions as a  
XX cytotoxic agent. The products can be used for selectively killing cells  
XX expressing a specific surface marker. They can be used for treating  
XX tumors or infected cells (e.g. cells infected by viruses (especially  
XX latent or chronic virus infections, such as human immunodeficiency virus  
XX (HIV)-1, Epstein-Barr virus, herpes viruses (herpes simplex types I and  
XX II), hepatitis viruses (B, non-A-non-B, and delta), herpes zoster, and  
XX cytomegalovirus) and cells infected with parasites (such as the malaria  
XX parasite)). They can also be used for treating immune dysfunctional cells  
XX in immune and autoimmune diseases. Additionally, they may be used as  
XX contraptives. Finally they can also be used for cell separation in  
XX vitro by selectively killing unwanted types of cells (e.g. in bone  
XX marrow) prior to transplantation into a patient undergoing marrow  
XX ablation by radiation or for killing leukemia cells or T-cells that would  
XX cause graft-versus-host disease. This sequence represents a bullfrog

CC N-terminal methionine due to the presence of a signal peptide that is  
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the  
 CC proteins to be fused in-frame with ligand binding moieties to form  
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and  
 CC autoimmune diseases

XX  
 SQ Sequence 110 AA;

Query Match 99.3%; Score 596; DB 2; Length 110;  
 Best Local Similarity 98.2%; Pred. No. 1.9e-59;  
 Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QNWATFOQKHIIINTPIICNTILDNNIYVGGCKRVNTFISSATTVAICTGVINLNL 60  
 Db 1 QNWATFOQKHIIINTPIICNTILDNNIYVGGCKRVNTFISSATTVAICTGVINLNL 60  
 QY 61 STTRFQMLTCTRTSITPRPCVSSRTETNYICVKCENQYPVHFAGIGRCP 110  
 Db 61 STTRFQMLTCTRTSITPRPCVSSRTETNYICVKCENQYPVHFAGIGRCP 110

## RESULT 4

AAZ28873  
 ID AAZ28873 standard; protein; 111 AA.  
 XX  
 AC AAZ28873;  
 XX  
 DT 25-JAN-2000 (first entry)  
 XX  
 DE Recombinant Met (-1) RaCOR1.

XX  
 KW Recombinant Met (-1) Rana catesbeiana oocyte ribonuclease; RaCOR1; CD22;  
 KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;  
 KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;  
 KW recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;  
 KW RNase; autoimmune disease.  
 XX

OS Rana catesbeiana.  
 OS Synthetic.

XX  
 PH Key Location/Qualifiers  
 FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"

XX WO9950398-A2.  
 XX 07-OCT-1999.  
 XX 26-MAR-1999; 99WO-US006641.  
 XX 27-MAR-1998; 98US-0079751P.  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Rybak SM, Newton DL;  
 XX WPI; 1999-610847/52.  
 XX N-PSDB; AAZ08131.

XX New recombinant ribonucleases, used for killing target cells, e.g. for  
 XX treating cancers, viral infections or autoimmune diseases.  
 XX Claim 22; Page 63; 71pp; English.

XX The present sequence is a recombinant Rana catesbeiana oocyte  
 XX ribonuclease (RaCOR1) protein with Met at position 1. Carboxy terminal  
 XX end of recombinant RaCOR1 has a covalently bound ligand binding moiety,  
 XX which can be a LL2 antibody directed against CD22 on cancerous B cells or  
 XX human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma  
 XX cells. Recombinant ribonucleases can be expressed in bacteria without an  
 XX N-terminal methionine due to the presence of a signal peptide that is  
 XX cleaved by bacteria. The soluble expression of ribonuclease allows the  
 XX proteins to be fused in-frame with ligand binding moieties to form

CC cytotoxic fusion proteins. They can be used for treatment of cancer and  
 CC autoimmune diseases  
 XX  
 SQ Sequence 111 AA;

Query Match 99.3%; Score 596; DB 2; Length 111;  
 Best Local Similarity 98.2%; Pred. No. 1.9e-59;  
 Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QNWATFOQKHIIINTPIICNTILDNNIYVGGCKRVNTFISSATTVAICTGVINLNL 60  
 Db 2 QNWATFOQKHIIINTPIICNTILDNNIYVGGCKRVNTFISSATTVAICTGVINLNL 61  
 QY 61 STTRFQMLTCTRTSITPRPCVSSRTETNYICVKCENQYPVHFAGIGRCP 110  
 Db 62 STTRFQMLTCTRTSITPRPCVSSRTETNYICVKCENQYPVHFAGIGRCP 111

## RESULT 5

AAZ28877  
 ID AAZ28877 standard; protein; 110 AA.  
 XX  
 AC AAZ28877;  
 XX  
 DT 25-JAN-2000 (first entry)  
 XX  
 DE Recombinant RaCOR1 Gln1Ser amino acid sequence.

XX  
 KW Recombinant Rana catesbeiana oocyte ribonuclease; RaCOR1 Gln1Ser; CD22;  
 KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;  
 KW bullfrog; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; RNase;  
 KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;  
 KW cancer; autoimmune disease.  
 XX

OS Rana catesbeiana.  
 OS Synthetic.

XX  
 PH Key Location/Qualifiers  
 FT Misc-difference 1 /note= "Wild type Gln replaced with Ser"

XX WO9950398-A2.  
 XX 07-OCT-1999.  
 XX 26-MAR-1999; 99WO-US006641.  
 XX 27-MAR-1998; 98US-0079751P.  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Rybak SM, Newton DL;  
 XX WPI; 1999-610847/52.  
 XX N-PSDB; AAZ08134.

XX New recombinant ribonucleases, used for killing target cells, e.g. for  
 XX treating cancers, viral infections or autoimmune diseases.  
 XX Claim 22; Page 67; 71pp; English.

XX The present sequence is a recombinant Rana catesbeiana oocyte  
 XX ribonuclease (RaCOR1) protein with Gln1Ser. Carboxy terminal end of  
 XX recombinant RaCOR1 has a covalently bound ligand binding moiety, which  
 XX can be a LL2 antibody directed against CD22 on cancerous B cells or human  
 XX chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.  
 XX Recombinant ribonucleases can be expressed in bacteria without an N-  
 XX terminal methionine due to the presence of a signal peptide that is  
 XX cleaved by bacteria. The soluble expression of ribonuclease allows the  
 XX proteins to be fused in-frame with ligand binding moieties to form  
 XX cytotoxic fusion proteins. They can be used for treatment of cancer and  
 XX autoimmune diseases



Sat May 8 17:57:17 2004

CC which can be a LL2 antibody directed against CD22 on cancerous B cells or  
CC human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma  
CC cells. Recombinant ribonucleases can be expressed in bacteria without an  
CC N-terminal methionine due to the presence of a signal peptide that is  
CC cleaved by bacteria. The soluble expression of ribonuclease allows the  
CC proteins to be fused in-frame with ligand binding moieties to form  
CC cytotoxic fusion proteins. They can be used for treatment of cancer and  
CC autoimmune diseases  
XX  
SQ Sequence 110 AA;

Query Match 100.0%; Score 600; DB 2; Length 110;  
Best Local Similarity 100.0%; Pred. No. 6.8e-60; Indels 0; Gaps 0;  
Matches 110; Conservative 0; Mismatches 0;  
QY 1 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLVL 60  
DB 1 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLVL 60  
QY 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYVHFAGIGRCP 110  
DB 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYVHFAGIGRCP 110

RESULT 2  
AA28876  
ID AAY28876 standard; protein; 111 AA.

AC AAY28876;  
DT 25-JAN-2000 (first entry)  
DE Recombinant Met (-1) RaCOR1 Met22Leu Met57Leu-(His)6 protein.  
KW Met (-1) Rana catesbeiana ribonuclease Met22Leu Met57Leu-(His)6; RaCOR1;  
KW recombinant; CD22; covalently bound; LL2 antibody; ligand binding moiety;  
KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;  
KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;  
KW cancer; bullfrog; RNase; autoimmune disease.  
XX Rana catesbeiana.  
OS Synthetic.

XX Key Location/Qualifiers  
FH Misc-difference 1 /note= "Met not found in wild type RaCOR1"  
FT Misc-difference 1 /note= "(His)6 histidine tag attached to N-terminal Met"  
FT Misc-difference 23 /note= "Wild type Met replaced with Leu"  
FT Misc-difference 58 /note= "Wild type Met replaced with Leu"

XX WO9950398-A2.  
XX 07-OCT-1999.  
XX 26-MAR-1999; 99WO-US006641.  
XX 27-MAR-1998; 98US-0079751P.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX Rybak SM, Newton DL;  
XX WPI; 1999-610847/52.  
XX N-PSDB; AA208130.  
XX New recombinant ribonucleases, used for killing target cells, e.g. for  
XX treating cancers, viral infections or autoimmune diseases.  
XX Claim 22; Page 66; 71pp; English.

CC The present sequence is a recombinant Rana catesbeiana oocyte  
CC ribonuclease (RaCOR1) protein with Met at position 1 attached to a (His)6  
CC tag, Met23Leu and Met58Leu. Carboxy terminal end of recombinant RaCOR1  
CC has a covalently bound ligand binding moiety, which can be a LL2 antibody  
CC directed against CD22 on cancerous B cells or human chorionic  
CC gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant  
CC ribonucleases can be expressed in bacteria without an N-terminal  
CC methionine due to the presence of a signal peptide that is cleaved by  
CC bacteria. The soluble expression of ribonuclease allows the proteins to  
CC be fused in-frame with ligand binding moieties to form cytotoxic fusion  
CC proteins. They can be used for treatment of cancer and autoimmune  
CC diseases  
XX  
SQ Sequence 111 AA;

Query Match 100.0%; Score 600; DB 2; Length 111;  
Best Local Similarity 100.0%; Pred. No. 6.8e-60; Indels 0; Gaps 0;  
Matches 110; Conservative 0; Mismatches 0;  
QY 1 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLVL 60  
DB 2 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLVL 61  
QY 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYVHFAGIGRCP 110  
DB 62 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYVHFAGIGRCP 111

RESULT 3  
AAY28872  
ID AAY28872 standard; protein; 110 AA.

AC AAY28872;  
DT 25-JAN-2000 (first entry)  
DE Rana catesbeiana oocyte ribonuclease (RaCOR1) amino acid sequence.  
KW Rana catesbeiana oocyte ribonuclease; RaCOR1; covalently bound; CD22;  
KW LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's Sarcoma;  
KW human chorionic gonadotrophin; hCG; recombinant ribonuclease; bullfrog;  
KW signal peptide; cytotoxic fusion protein; cancer; autoimmune disease;  
KW RNase.

XX Rana catesbeiana.  
OS Synthetic.  
XX WO9950398-A2.  
XX 07-OCT-1999.  
XX 26-MAR-1999; 99WO-US006641.  
XX 27-MAR-1998; 98US-0079751P.  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Rybak SM, Newton DL;  
XX WPI; 1999-610847/52.  
XX N-PSDB; AA208130.  
XX New recombinant ribonucleases, used for killing target cells, e.g. for  
XX treating cancers, viral infections or autoimmune diseases.  
XX Claim 22; Page 62; 71pp; English.

XX The present sequence is a Rana catesbeiana oocyte ribonuclease (RaCOR1)  
XX protein encoded by a cDNA modified for expression in E. coli. Carboxy  
XX terminal end of RaCOR1 has a covalently bound ligand binding moiety,  
XX which can be a LL2 antibody directed against CD22 on cancerous B cells or  
XX human chorionic gonadotrophin (hCG) effective against Kaposi's Sarcoma  
XX cells. Recombinant ribonucleases can be expressed in bacteria without an  
XX cells.

Result No.	Query			ID	Description
	No.	Score	Match		
1	600	100.0	110	2	AAY28874
2	600	100.0	111	2	AAY28876
3	596	99.3	110	2	AAY28872
4	596	99.3	111	2	AAY28873
5	591	98.5	110	2	AAY28877
6	591	98.5	111	2	AAY28878
7	582.5	97.1	111	2	AAY33321
8	280.5	46.8	104	2	AAW05544
9	279.5	46.6	104	2	AAW28866
10	279.5	46.6	105	2	AAY28869
11	277.5	46.2	104	2	AAY28865
12	277.5	46.2	105	2	AAY28867
13	277.5	46.2	127	2	AAY28879
14	273.5	45.6	104	2	AAW30301
15	273.5	45.6	104	4	AAB311667
16	273.5	45.6	104	4	AAB311666
17	273.5	45.6	104	5	ABG32650
18	273.5	45.6	104	5	ABG31617
19	273.5	45.6	105	5	ABG32650
20	273.5	45.6	379	2	AAW39400
21	272.5	45.4	104	2	AAW35126
22	272.5	45.4	104	2	AAW30302
23	272.5	45.4	104	2	AAY28870
24	270.5	45.1	104	2	AAY28871
25	270.5	45.1	104	2	AAAR12344
					AAAR47303

The present sequence is a recombinant *Rana catesbeiana* oocyte ribonuclease (RaCOR1) protein with Met22Leu/Met57Leu. Carboxy terminal end of recombinant RaCOR1 has a covalently bound ligand binding moiety.

RA Beintema J.J.;  
RT "Secretory ribonuclease genes and pseudogenes in true ruminants.";  
RL Gene 212:259-268(1998).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC -----  
DR EMBL; Y11670; CAA72368.1; -.  
DR HSSP; P00656; ISRN.  
DR InterPro; IPR001427; RNaseA.  
DR Pfam; PF00074; rna5a; 1.  
DR PRINTS; PR00794; RIBONUCLEASE.  
DR ProDom; PD000535; RNaseA; 1.  
DR SMART; SM00092; RNasePc; 1.  
DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.  
FT ACT SITE 41 41 BY SIMILARITY.  
FT DISULFID 26 84 BY SIMILARITY.  
FT DISULFID 40 95 BY SIMILARITY.  
FT DISULFID 58 110 BY SIMILARITY.  
FT DISULFID 65 72 BY SIMILARITY.  
FT CARBOHYD 62 62 N-LINKED (GLCNAC...) (BY SIMILARITY).  
FT CARBOHYD 129 129 O-LINKED (BY SIMILARITY).  
FT CARBOHYD 133 133 O-LINKED (BY SIMILARITY).  
SQ SEQUENCE 151 AA; 16819 MW; E95F3757FFCSB233 CRC64;

Query Match 21.0%; Score 127.5; DB 1; Length 151;  
Best Local Similarity 30.6%; Pred. No. 8.5e-07;  
Matches 37; Conservative 17; Mismatches 44; Indels 23; Gaps 7;

QY 5 ATFOOKHI-----INTPIICNTIMDNNTIYVGGQCKRYNTFISSATTWKAITGVNN 58  
Db 6 AKFRQHM DAGSSSGNSNYCNQMKER-PMTHGRCKPVNTFVHESLDSVKAVCS---QK 61  
QY 59 NVL-----STTRFOLNCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFA 105  
Db 62 NITCKNGQPCYQSNSTMTNITDRETGSSKYPNCAYKTSQKQKYITVACEGNPYVPVHFD 121  
QY 106 G 106  
Db 122 G 122

Search completed: May 7, 2004, 21:53:06  
Job time : 6.60711 secs



Sat May 8 17:57:16 2004

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OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidæ; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_SEQUENCE.
RP SEQUENCE.
RC TISSUE=Wilk, and Serum; PubMed=9256695;
RX MEDLINE=97409980; PubMed=9256695;
RA Strödom D.J., Bond M.D., Vallee B.L.;
RT "An angiogenic protein from bovine serum and milk -- purification and
RT primary structure of angiogenin-2."
RL Eur J Biochem. 247:535-544(1997).
CC -!- FUNCTION: Binds tightly to placental ribonuclease inhibitor and
CC has very low ribonuclease activity. Has potent angiogenic
CC activity. Angiogenin induces vascularization of normal and
CC malignant tissues. Abolishes protein synthesis by specifically
CC hydrolyzing cellular tRNAs.
CC -!- TISSUE SPECIFICITY: Serum and milk.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC HSSP; P10152; IAGI.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW Protein synthesis inhibitor; Glycoprotein;
KW Pyrolidone carboxylic acid.
FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 39 39 BY SIMILARITY.
FT ACT_SITE 113 113 BY SIMILARITY.
FT DISULFID 25 80
FT DISULFID 38 91
FT DISULFID 56 106
FT CARBOHYD 33 33 N-LINKED (GLCNAC...) (BY SIMILARITY).
SQ SEQUENCE 123 AA; 14522 MW; B703B9839919FD2F CRC64;

Query Match 21.0%; Score 127.5; DB 1; Length 123;
Best Local Similarity 30.6%; Pred. No. 6.9e-07;
Matches 33; Conservative 19; Mismatches 43; Indels 13; Gaps 5;

Qy 7 PQKHINTPI-----ICNTMDNNIYVGGCKRVNTFISSATTVKAIK---TGVINM 58
Db 8 FLRKHDPGCHDDRYCNTMWER--NTPRCKDNTNFIHGNSDDIRAVCDRNGEYR 65
Qy 59 NVLSTTR--FQNLCTRTSITPR-PCPYSSRTETNYICVKENQYVPH 103
Db 66 NGLRSRSPFQVTTCTHRGSRPFCRYRFRANRVIVIRCDRGFFIH 113

RESULT 14
RNBR GIRCA STANDARD; PRT; 141 AA.
AC Q29542; Q29533;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ribonuclease, brain (BC 3.1.27.-) (BRB).
GN BRN.
OS Giraffa camelopardalis (Giraffe).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Giraffoidea;
OC Giraffidae; Giraffa.
OX NCBI_TaxID=9894;
RN [1]_SEQUENCE FROM N.A.
RP MEDLINE=96139017; PubMed=8587129;
RX Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
RA Vento M.T., Furia A.;
RA "Molecular evolution of genes encoding ribonucleases in ruminant
RT species."
RT J. Mol. Evol. 41:850-858(1995).

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RN SEQUENCE OF 31-114 FROM N.A.
RP MEDLINE=93367815; PubMed=8360916;
RX Breukelman H.J., Beintema J.J., Confalone E., Costanzo C., Sasso M.P.,
RA Carsana A., Palmieri M., Furia A.;
RT "Sequences related to the ox pancreatic ribonuclease coding region in
RT the genomic DNA of mammalian species."
RL J. Mol. Evol. 37:29-35(1993).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC EMBL; S81743; AAB36137.1; -.
DR EMBL; S65126; AAB27931.1; -.
DR HSSP; P00656; 2RNS.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR Hydrolase; Nuclease; Endonuclease; Glycoprotein.
KW ACT_SITE 41 41 BY SIMILARITY.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT CARBOHYD 62 62 N-LINKED (GLCNAC...) (BY SIMILARITY).
FT CARBOHYD 129 129 O-LINKED (BY SIMILARITY).
SQ SEQUENCE 141 AA; 15592 MW; 73745EFE9079591F CRC64;

Query Match 21.0%; Score 127.5; DB 1; Length 141;
Best Local Similarity 30.6%; Pred. No. 7.9e-07;
Matches 37; Conservative 17; Mismatches 44; Indels 23; Gaps 7;

Qy 5 ATFOQKH-----INTPLICTMDNNIYVGGCKRVNTFISSATTVKAICTGVINM 58
Db 6 AKFRQHMDSGSSSSNSNYCNQMKR-RMTHRCRFPVNTFVHESLADKAVCS---QK 61
Qy 59 NVL-----STTRFQLNCTRTSITPR-PCPYSSRTETNYICVKE-NQY-PVHFA 105
Db 62 NITCKGQPCYQSNSTMNITDCTGTGSSKYPNCAYKTSQKQYITVACEGNPYVPVHED 121
Qy 106 G 106
Db 122 G 122

RESULT 15
RNBR AXIPR STANDARD; PRT; 151 AA.
AC P87350;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease, brain (BC 3.1.27.-) (BRB).
GN BRN.
OS Axis porcinus (Hog deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Cervinae; Axis.
OX NCBI_TaxID=57737;
RN [1]_SEQUENCE FROM N.A.
RP MEDLINE=98278842; PubMed=9611269;
RX Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,
RA

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SQ SEQUENCE      124 AA;   13804 MW;   OAC28CDEI4111845 CRC64;

Query Match
Best Local Similarity    31.6%; Score 132.5; DB 1; Length 124;
Matches       36; Conservative     19; Mismatches    42; Indels    17; Gaps      6;


QY      7 FQQKHI-----INTPIICNTIMDNNVIVGGCKRVNVTFTISSATTVKAICTGV-INNM 59
           |||::|| :||:||||:||||:||||:||||:||||:||||:||||:||||:
Dd      8 FQGHWDPSSSNSSNSNYCNLMWSRR-NWTOGRCKPVPVTFVESLADVOVCQSINQVK 66
           |||::|| :||:||||:||||:||||:||||:||||:||||:||||:||||:

QY      60 VLSTTRFQLT-----CTRISITPRP-CPYSSRSTETNIYICKVENO--YPVFH 104
           |||::|| :||:||||:||||:||||:||||:||||:||||:||||:||||:
Dd      67 NGQTNCYGSNSTMHTIDCRGTGSSKYPCAYKASQEOKHIIIVACEGNPPFPVVHF 120
           |||::|| :||:||||:||||:||||:||||:||||:||||:||||:||||:



RESULT 11
RNP_IGUIG
ID_RNP_IGUIG STANDARD; PRT; 119 AA.
AC PF0287;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase A).
OS Iguana iguana (Common Iguana).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguanua; Iguanidae; Iguaninae; Iguana.
OX NCBI_TaxID=8517;
RN [1]
RP SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=94139745; PubMed=8307028;
RA Zhao W., Beintema J.J., Hofsteenge J.;
RT "The amino acid sequence of iguana (Iguana iguana) pancreatic
RT ribonuclease.";
RL Eur. J. Biochem. 219:641-646(1994).
CC -! CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -! SUBCELLULAR LOCATION: Secreted.
CC -! TISSUE SPECIFICITY: Pancreas.
CC -! SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR PIN; S4111; S4111.
DR HSHP; PD0656; ILSQ.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PR00074; rnaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SN00092; RNAse PC; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
KW Hydroxylase; Nuclease; Endonuclease; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 25 80 BY SIMILARITY.
FT FT 39 91 BY SIMILARITY.
FT DISULFID 57 106 BY SIMILARITY.
FT ACT_SITE 10 10 BY SIMILARITY.
FT ACT_SITE 40 40 BY SIMILARITY.
FT ACT_SITE 113 113 BY SIMILARITY.
SQ SEQUENCE      119 AA;   13324 MW;   6072FB5B7B15BD5A CRC64;

Query Match
Best Local Similarity    30.4%; Score 131.5; DB 1; Length 119;
Matches       35; Conservative     16; Mismatches    51; Indels    13; Gaps      4;


QY      2 QNWATEFOQH-----INFPICNTIMDNVIYGCGCKRVNVTFTISSATTVAIC-- 52
           |:::||| ::|||:||||:||||:||||:||||:||||:||||:||||:
Dd      1 QDWSSFQNKHDIPETSASFNFNAVCGLMMQR-LNLPTKCTKTNTFWHASPFIQQVGCS 59
           |:|::||| ::|||:||||:||||:||||:||||:||||:||||:||||:

QY      53 --TGVINMVLSITFLQNTCTRSIT-PRPCPSYSTETNIYCIVENQPYPHF 104
           ||::||| ::|||:||||:||||:||||:||||:||||:||||:||||:
Dd      60 GGTHEDLNLYDSNESFDLTDCKNVGGTAPSCSKNGTPGTKRIACENNOPWHF 114
           ||::||| ::|||:||||:||||:||||:||||:||||:||||:||||:



RESULT 12
```

16-OCT-2001 (Rel. 40, Last annotation update)  
Ribonuclease, brain precursor (EC 3.1.27.-) (BRB).  
BRN.  
Bos taurus (Bovine).  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae;  
Bovidae; Bovinae; Bos.  
NCBI\_TaxID=9913;  
[1]  
SEQUENCE FROM N.A.  
MEDLINE=92093604; PubMed=1754384;  
Sasso M.P., Carsana A., Confalone E., Cosi C., Sorrentino S.,  
Viola M., Palmieri M., Russo E., Furia A.;  
"Molecular cloning of the gene encoding the bovine brain ribonuclease  
and its expression in different regions of the brain.";  
Nucleic Acids Res. 19:6469-6474(1991).  
[2]  
SEQUENCE OF 27-167, AND CARBOHYDRATE-LINKAGE SITES.  
TISSUE=Brain;  
MEDLINE=89214015; PubMed=3243767;  
Watanabe H., Kato H., Ishii M., Komoda Y., Sanda A., Takizawa Y.,  
Ohgi K., Irie M.;  
"Primary structure of a ribonuclease from bovine brain.";  
J. Biochem. 104:939-945(1988).  
[3]  
SEQUENCE OF 27-167 FROM N.A.  
MEDLINE=96139017; PubMed=8587129;  
Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,  
Vento M.T., Furia A.;  
"Molecular evolution of genes encoding ribonucleases in ruminant  
species.";  
J. Mol. Evol. 41:850-858(1995).  
C -1- SUBCELLULAR LOCATION: Secreted.  
C -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
C  
C This SWISS-PROT entry is copyright. It is produced through a colla-  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).  
C  
C  
C EMBL; X59767; CA942439.1; -;  
C EMBL; S81744; AAB36138.1; -;  
C PIR; S20066; S20066.  
C HSP; P00656; 2RNS.  
C GlycoSuiteDB; P39873; -;  
C InterPro; IPR001427; RNaseA.  
C Pfam; PF00074; rnaseA; 1.  
C PRINTS; PR00794; RIBONUCLEASE.  
C ProDom; PD000535; RNaseA; 1.  
C SMART; SM00092; RNase\_Pc; 1.  
C PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
C Hydrolase, Nuclease; Endonuclease; Glycoprotein; Signal.  
C  
C SIGNAL  
C 1 26  
C CHAIN 27 167 RIBONUCLEASE, BRAIN.  
C ACT SITE 38 38 BY SIMILARITY.  
C ACT SITE 67 67 BY SIMILARITY.  
C ACT SITE 145 145 BY SIMILARITY.  
C DISULFID 52 110 BY SIMILARITY.  
C DISULFID 66 121 BY SIMILARITY.  
C DISULFID 84 136 BY SIMILARITY.  
C DISULFID 91 98 BY SIMILARITY.  
C CARBOHYD 88 88 N-LINKED (GLCNAC...).  
C  
C CARBOHYD 155 155 O-LINKED.  
C CARBOHYD 159 159 O-LINKED.  
C FT CONFLICT 155 155 T -> S (IN REF. 2).  
C SEQUENCE 167 AA; 18450 MW; 681CAAC3CC2FC459 CRC64;  
SQ  
Query Match 22.0%; Score 133.5; DB 1; Length 167;  
Best Local Similarity 31.4%; Pred. No. 2.1e-07;  
Query Match 22.0%; Score 133.5; DB 1; Length 167;  
Best Local Similarity 31.4%; Pred. No. 2.1e-07;

Matches	38;	Conservative	17;	Mismatches	43;	Indels	23;	Gaps	7;
QY	5	ATFOQKHI-----INTPLCNTMDNNIYIVGGCKRVNTFISSATTVKAICTGVNM	58						
DB	32	AKFRQHMDSGSSSSNPNYCNQMKRR-RMTHGCKPNTVFHESLDDVKAVCS---QK	87						
QY	59	NVL-----STTRFQLNTCTRTSITPRP-CPYSSRTENYICVKE-NQY-PVHFA	105						
DB	88	NITKNGHPNCYQSKSTSIITDRETGSSKYDNCAYKTSQKQKIITVACEGPNYPVPHF	147						
QY	106	G 106							
DB	148	G 148							

  

RESULT 10	
RNP_PIG	STANDARD; PRT; 124 AA.
ID - RNP_PIG	
AC P00671;	
DT 21-JUL-1986 (Rel. 01, Created)	
DT 21-JUL-1986 (Rel. 01, Last sequence update)	
DT 28-FEB-2003 (Rel. 41, Last annotation update)	
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).	
DE RNASE1 OR RNS1.	
OS Sus scrofa (Pig).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.	
OC NCBI_Taxid:9823;	
RN [1]	
RN RP	
RN MEDLINE=70104197; PubMed=5460946;	
RA Jackson R.L., Hirs C.H.W.;	
RA "The primary structure of porcine pancreatic ribonuclease. II. The	
RT amino acid sequence of the reduced S-aminoethylated protein.";	
RT J. Biol. Chem. 245:637-653 (1970).	
RN [2]	
RN RP	
RN REVISION TO 2.	
RA Wierenga R.K., Huizinga J.D., Gaastra W., Welling G.W., Beintema J.J.;	
RA "Affinity chromatography of porcine pancreatic ribonuclease and	
RT reinvestigation of the N-terminal amino acid sequence.";	
RT FEBS Lett. 31:181-185 (1973).	
RN [3]	
RN RP	
RN DISULFIDE BONDS.	
EX MEDLINE=70104198; PubMed=4904878;	
RA Phelan J.J., Hirs C.H.W.;	
RA "The primary structure of porcine pancreatic ribonuclease. 3. The	
RT disulfide bonds.";	
RT J. Biol. Chem. 245:654-661 (1970).	
CC 1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-	
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P	
CC with 2',3'-cyclic phosphate intermediates.	
CC -1- SUBCELLULAR LOCATION: Secreted.	
CC -1- TISSUE SPECIFICITY: Pancreas.	
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.	
DR PIR; A92071; NRPG.	
DR HSP; P00656; 1SRN.	
DR InterPro; IPR001427; RNaseA.	
DR Pfam; PF00074; rnaaseA; 1.	
DR PRINTS; PR00794; RIBONUCLEASE.	
DR ProDom; PD000535; RNaseA; 1.	
DR SMART; SM00092; RNase PG; 1.	
DR PROSITE; PS00127; RNASE PANCREATIC; 1.	
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.	
FT DISULFID 26 84	
FT DISULFID 40 95	
FT DISULFID 58 110	
FT DISULFID 65 72	
FT ACT_SITE 12 12	
FT ACT_SITE 41 41	
FT ACT_SITE 119 119	
FT CARBOHYD 21 21	
FT CARBOHYD 34 34	
FT CARBOHYD 76 76	

  

BY SIMILARITY.	
BY SIMILARITY.	
BY SIMILARITY.	
N-LINKED (GLCNAC. .)	
N-LINKED (GLCNAC. .)	
N-LINKED (GLCNAC. .)	

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DR PIR; A00818; NRWHK.
DR HSP; P00656; LSRN.
DR InterPro: IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA.1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA.1.
DR SMART; SM00092; RNase Pc; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
KW Hydroxylase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84
FT DISULFID 40 95
FT DISULFID 58 110
FT DISULFID 65 72
FT ACT_SITE 12 12
FT ACT_SITE 41 41
FT ACT_SITE 119 119
FT CARBOHYD 76
SQ SEQUENCE 124 AA; 14125 MW; F57475459F697E20 CRC64;

Query Match 22.3%; Score 135.5; DB 1; Length 124;
Best Local Similarity 33.3%; Pred. No. 9.5e-08;
Matches 39; Conservative 16; Mismatches 39; Indels 23; Gaps 7;

QY 7 FQKHII-----NTPILCNTMDNNIVIGSOCKRVNTFISSATTVKAICTGVNNV 60
Db 8 FQKHMDSGNSPGNNVYCNQMMRR-KNTQCKPKVNTFVHESLEDYKAVCS---QKNV 63
QY 61 I-----STTRFQNTCTRTSITPRP-CPYSSRTETNYICVKE-NOY-PVHF 104
Db 64 LCKNGRTNVCYNSMTHTDCRQSGSKYPNCAKYSQKEHIIIVACEGNYVPVHF 120

RESULT 8
ID ANGI_MOUSE STANDARD; PRT; 145 AA.
AC P21570;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Angiogenin precursor (EC 3.1.1.27.-) (Ribonuclease 5) (RNase 5).
GN ANG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RX MEDLINE=91025023; PubMed=2222458;
RA Bond M.D., Vallee B.L.;
RT "Isolation and sequencing of mouse angiogenin DNA.";
RL Biochem. Biophys. Res. Commun. 171:988-995(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.G., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length

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RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP PARTIAL SEQUENCE.
RX TISSUE=Serum;
RC MEDLINE=93192291; PubMed=8448182;
RA Bond M.D., Strydom D.J., Vallee B.L.;
RT "Characterization and sequencing of rabbit, pig and mouse
angiogenins: discernment of functionally important residues and
regions.";
RL Biochim. Biophys. Acta 1162:177-186(1993).
CC -!- FUNCTION: May function as a tRNA-specific ribonuclease that binds
to actin on the surface of endothelial cells; once bound,
angiogenin is endocytosed and translocated to the nucleus, thereby
promoting the endothelial invasiveness necessary for blood vessel
formation. Angiogenin induces vascularization of normal and
malignant tissues. Abolishes protein synthesis by specifically
hydrolyzing cellular tRNAs.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U22516; AAA91366.1; -.
DR EMBL; BC055355; AAH55355.1; -.
DR PIR; A35932; A35932.
DR HSP; P03950; 1A4Y.
DR MGD; MGI:88022; Ang.
DR InterPro: IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA.1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA.1.
DR SMART; SM00092; RNase Pc; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
KW Hydroxylase; Nuclease; Endonuclease; Angiogenesis;
KW Protein synthesis inhibitor; Signal; Pyroliadone carboxylic acid.
FT SIGNAL 1 24
FT CHAIN 25 145
FT MOD_RES 25 25
FT ANGIOENIN.
PYRROLIDONE CARBOXYLIC ACID (BY
SIMILARITY).
FT ACT_SITE 37 37
FT ACT_SITE 64 64
FT ACT_SITE 137 137
FT DISULFID 50 104
FT DISULFID 63 115
FT DISULFID 81 130
FT SEQUENCE 145 AA; 16228 MW; 06944260BB764938 CRC64;
SQ SEQUENCE 145 AA; 16228 MW; 06944260BB764938 CRC64;

Query March 22.3%; Score 135.5; DB 1; Length 145;
Best Local Similarity 39.5%; Pred. No. 1.1e-07;
Matches 30; Conservative 12; Mismatches 29; Indels 5; Gaps 3;

QY 34 CKRVNTFFIISATTVKAIC---TGVNNV-LSTTRFQNTCTRTSITPR-PCPYSSRTE 88
Db 63 CKDVNTFFHGNKSNKKAICGANGSPYRNLKMSKFPQVTTCKTGSPRPCCYRASAG 122
QY 89 TNYICVKEQNPVHF 104
Db 123 FRHVVIACENGLPVHF 138

RESULT 9
RNER_BOVIN
ID RNER_BOVIN STANDARD; PRT; 167 AA.
AC P39873;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)

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RL J. Biochem. 106:729-735 (1989).  
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-  
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P  
 CC with 2',3'-cyclic phosphate intermediates.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
 DR PIR; JX0085; JX0085.  
 DR HSSP; P11916; LBC4.  
 DR InterPro; IPR001427; RNaseA.  
 DR Pfam; PF00074; RNaseA; 1.  
 DR ProDom; PD000535; RNaseA; 1.  
 DR SMART; SM00092; RNase PC; 1.  
 DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
 KW Hydrolase; Nuclease; Endonuclease; Pyridolone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT ACT\_SITE 10 10  
 FT ACT\_SITE 35 35 BY SIMILARITY.  
 FT ACT\_SITE 104 104 BY SIMILARITY.  
 FT DISULFID 19 72 BY SIMILARITY.  
 FT DISULFID 34 82 BY SIMILARITY.  
 FT DISULFID 52 97 BY SIMILARITY.  
 FT DISULFID 94 111 PROBABLE.  
 SQ SEQUENCE 111 AA; 12461 MW; D64BA72456C10788 CRC64;  
 Query Match 61.6%; Score 374; DB 1; Length 111;  
 Best Local Similarity 65.8%; Pred. No. 1.9e-33;  
 Matches 73; Conservative 9; Mismatches 27; Indels 2; Gaps 2;  
 QY 2 QNWATFOQKHINTPII-CNTIMDNNIYVGGQCKRVNTFIISATTVKAICTGVI-NMN 59  
 Db 1 QNWAKFKKHIRSTSSDCNTIMDKAIYVGGCKERTNFIISDENVKICSGVSPDRK 60  
 QY 60 VLSSTFRFQNTCTTSITPRPCYSSTRTETNYICVCKENQYPVHFAGIGRC 110  
 Db 61 ELSTTSFKNTCTRDSITPRPCYPHPSPDNNKICVCKEQLPVHFVIGKC 111  
 RESULT 4  
 RN30\_RANPI STANDARD; PRT; 104 AA.  
 AC P22069;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE P-30 protein (EC 3.1.27.-) (Onconase).  
 OS Rana pipiens (Northern leopard frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8404;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Embryo;  
 RX MEDLINE=91093131; PubMed=1985896;  
 RA Ardelit W., Mikulski S.M., Shogen K.;  
 RT "Amino acid sequence of an anti-tumor protein from Rana pipiens  
 RT oocytes and early embryos. Homology to pancreatic ribonucleases.";  
 RL J. Biol. Chem. 266:245-251 (1991).  
 RN [2]  
 RP 3D-STRUCTURE MODELING.  
 RX MEDLINE=93066156; PubMed=1438177;  
 RA Mosmann S.C., Johns K.L., Ardelit W., Mikulski S.M., Shogen K.,  
 RA James M.N.G.;  
 RT "Comparative molecular modeling and crystallization of P-30 protein:  
 RT a novel antitumor protein of Rana pipiens oocytes and early  
 RT embryos.";  
 RL Proteins 14:392-400 (1992).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).  
 RX MEDLINE=94166079; PubMed=8120892;  
 RA Mosmann S.C., Ardelit W., James M.N.G.;  
 RA "Refined 1.7 A X-ray crystallographic structure of P-30 protein, an  
 RT amphibian ribonuclease with anti-tumor activity.";  
 RL J. Mol. Biol. 236:1141-1153 (1994).

CC -1- FUNCTION: Basic protein with antiproliferative/cytotoxic activity  
 CC against several tumor cell lines in vitro, as well as antitumor  
 CC in vivo. It exhibits a ribonuclease-like activity against high  
 CC molecular weight ribosomal RNA.  
 CC -1- DEVELOPMENTAL STAGE: Early embryos (up to four blastomere stage).  
 CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
 DR PDB; 1ONC; 31-JAN-94.  
 DR InterPro; IPR001427; RNaseA.  
 DR Pfam; PF00074; RNaseA; 1.  
 DR ProDom; PD000535; RNaseA; 1.  
 DR SMART; SM00092; RNase PC; 1.  
 DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
 KW Hydrolase; Nuclease; Endonuclease; 3D-structure;  
 KW Pyridolone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT ACT\_SITE 10 10  
 FT ACT\_SITE 31 31  
 FT ACT\_SITE 97 97  
 FT DISULFID 19 68  
 FT DISULFID 30 75  
 FT DISULFID 48 90  
 FT DISULFID 87 104  
 FT HELIX 3 10  
 FT STRAND 11 12  
 FT HELIX 19 22  
 FT TURN 23 24  
 FT TURN 26 30  
 FT STRAND 33 38  
 FT HELIX 41 45  
 FT HELIX 46 48  
 FT TURN 49 50  
 FT STRAND 55 58  
 FT STRAND 63 70  
 FT TURN 74 75  
 FT STRAND 77 84  
 FT STRAND 86 91  
 FT TURN 92 93  
 FT STRAND 94 101  
 SQ SEQUENCE 104 AA; 11845 MW; 22A753C2F9E566B4 CRC64;  
 Query Match 45.7%; Score 277.5; DB 1; Length 104;  
 Best Local Similarity 49.5%; Pred. No. 4.2e-23;  
 Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;  
 QY 2 QNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFIISATTVKAICTGVI-NMN 59  
 Db 1 QDWLTFOKKHITNTRDVCDCNIMSTNLF----HCKKNFTIYGRPEPVKRAICKGIIASKN 56  
 QY 60 VLSSTFRFQNTCTTSITPRPCYSSTRTETNYICVCKENQYPVHFAGIGRC 110  
 Db 57 VLTTSEFYLSDC---NVTSPCKYKLUKSTNKFVTCVNCQAPVHFVGVGSC 104  
 RESULT 5  
 ANG3\_MOUSE STANDARD; PRT; 145 AA.  
 ID ANG3\_MOUSE  
 AC P97802;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Angiogenin-3 precursor (EC 3.1.27.-) (Angiogenin-related protein 2)  
 DE (EF-5).  
 GN ANG3 OR ANGL.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=97184476; PubMed=9032278;  
 RA Fu X., Kamps M.P.;  
 RT "E2a-Fbx1 induces aberrant expression of tissue-specific and

residues with a 3' flanking guanine. Hydrolyzes poly(U) and poly(C) as substrates, and prefers the former. The S-lectins in frog eggs may be involved in the fertilization and development of the frog embryo. This lectin agglutinates various animal cells, including normal lymphocytes, erythrocytes, and fibroblasts of animal and human origin. It is cytotoxic against several tumor cells.

-- SUBUNIT: Monomer.

-- SUBCELLULAR LOCATION: Secreted.

-- SIMILARITY: Belongs to the pancreatic ribonuclease family.

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-----C
EMBU; AF039104; AAD10702.1; -.
PIR; A27121; A27121.
PDB; 1BC4; 28-OCT-98.
PDB; 1M07; 21-JAN-03.
InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNase PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure;
Signal; Pyrrolidone carboxylic acid.
Signal 1 22
T CHAIN 23 133 RIBONUCLEASE, OOCYTES.
T MOD RES 23 23 PYRROLIDONE CARBOXYLIC ACID.
T ACT SITE 32 32
T ACT_SITE 57 57
T ACT_SITE 125 125
T DISULFID 41 93
T DISULFID 56 103
T DISULFID 74 118
T DISULFID 115 132
T HELIX 25 32
T HELIX 41 45
T TURN 48 49
T STRAND 59 63
T HELIX 67 73
T TURN 74 74
T STRAND 79 84
T STRAND 90 95
T STRAND 105 110
T STRAND 114 119
T STRAND 120 121
T TURN 122 129
SEQUENCE 133 AA; 14762 MW; A7D62594F7D1D16FOC CRC64;
ISO

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[illegible]

Sialic acid-binding lectin (EC 3.1.1.27.-).  
Rana japonica (Japanese reddish frog).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AMphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
NCBI TaxID=8402;  
[1]\_TaxID=  
RN SEQUENCE, AND DISULFIDE BONDS.  
RP  
RC TISSUE=Egg;  
RX MEDLINE=91035319; PubMed=2229005;  
RA Kamiya Y., Oyama F., Oyama K., Sakakibara F., Nitta K., Kawauchi H.,  
Takayanagi Y., Titani K.;  
RA "Amino acid sequence of a lectin from Japanese frog (*Rana japonica*)  
RT egg6.";  
RL J. Biochem. 108:139-143(1990).  
CC -!- FUNCTION: The S-lectins in frog eggs may be involved in the  
fertilization and development of the frog embryo. This lectin  
preferentially agglutinates a large variety of tumor cells, but it  
does not agglutinate non-transformed cells and erythrocytes.  
CC  
CC -!- SUBUNIT: Monomer.  
CC  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC  
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
DR PIR; JX0120; JX0120.  
DR HSP; P11916; LBC4.  
DR InterPro; IPR001427; RNaseA.  
DR Pfam; PF00074; rnasea; 1.  
DR ProDom; PD000535; RNaseA; 1.  
DR SMART; SM00092; RNase\_Pc; 1.  
DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
KW Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin;  
KW Pyridolone carboxylic acid.  
FT MOD\_RES 1  
FT ACT\_SITE 1  
FT ACT\_SITE 10  
FT ACT\_SITE 35  
FT ACT\_SITE 104  
FT ACT\_SITE 104  
FT DISULFID 19  
FT DISULFID 72  
FT DISULFID 34  
FT DISULFID 82  
FT DISULFID 52  
FT DISULFID 97  
FT DISULFID 94  
FT DISULFID 111  
FT SEQUENCE 111 AA; 12326 MW; FDEBDF3834ED679 CRC64;

	Query Match	75.0%;	DB 1;	Length 111;
	Best Local Similarity	78.4%;	Score 455;	Pred No. 3.7e-42;
	Matches	87;	Conservative	7; Mismatches 15; Indels 2; Gaps 2;
2	QNWATQQKHINTP	II	NTIMNNIYIVGQCKRVNTEFI	ISSATVKAICTGV-INNN 59
2y				
2b				
1	QNWATQEQKHINT	NS	INIMDKSIYIVGQCKERNTEFI	ISSATVKAICSGASTNRN 60
1y				
1b				
60	VLSTTFQLNCTRTS	IT	PRCPYSSRSTETNIVCVKCNQYPVHFA	GRC 110
60y				
60b				
61	VLSTTFQLNCTIR	SA	DRCPYNSRSTETNIVCVKCNRLPVHFA	IGRC 111
61y				
61b				

RESULT 3	NRNPL_RANCA	STANDARD;	ERT;	111 AA.
ID	NRNPL_RANCA			
AC	P14626;			
AD	01-APR-1990 (Rel. 14, Created)			
AE	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DD	Ribonuclease, liver (EC 3.1.27.5).			
DE	Rana catesbeiana (Bull frog).			
OS	Rana catesbeiana (Bull frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	NCBI_TaxID=8400;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Liver;			
RX	MEDLINE=90130374; PubMed=2613682;			
RA	Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,			
RA	Okazaki T., Ohgi K., Irie M.;			
RT	"Primary structure of a ribonuclease from bullfrog ( <i>Rana catesbeiana</i> )			
RT	liver."			

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:30:40 ; Search time 5.60711 Seconds  
(without alignments)  
1030.796 Million cell updates/sec

Title: US-09-961-400-17

Perfect score: 607

Sequence: 1 MQNWATFQKHIIPTICN.....ICVKENQYVHFAGIGRCP 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	591.5	97.4	133	1	RNPO_RANCA
2	455	75.0	111	1	LECS_RANJA
3	374	61.6	111	1	RNPL_RANCA
4	277.5	45.7	104	1	RN30_RANPI
5	154.5	25.5	145	1	ANGR_MOUSE
6	149.5	24.6	145	1	ANGR_MOUSE
7	135.5	22.3	124	1	RNP_BALAC
8	135.5	22.3	124	1	ANGI_MOUSE
9	133.5	22.0	167	1	RNBR_BOVIN
10	132.5	21.8	124	1	RNP_FIG
11	131.5	21.7	119	1	RNP_IGUIG
12	128.5	21.2	151	1	RNBR_CAPCA
13	127.5	21.0	123	1	ANG2_BOVIN
14	127.5	21.0	141	1	RNBR_GIRCA
15	127.5	21.0	151	1	RNBR_AXIPR
16	125	20.6	146	1	ANGI_SAISC
17	124	20.4	146	1	ANGI_MIOIA
18	123.5	20.3	143	1	RNBR_SHEEP
19	122.5	20.2	124	1	RNP_ANTAM
20	122.5	20.2	146	1	ANGI_CERAE
21	122	20.1	122	1	RNP_MACRU
22	120.5	19.9	128	1	RNP_MYOCO
23	120.5	19.9	149	1	RNP_MOUSE
24	120	19.8	146	1	ANGI_AOTTR
25	120	19.7	147	1	ANGI_PONFY
26	119.5	19.7	123	1	ANGI_PIG
27	118.5	19.5	128	1	RNFB_CAVPO
28	118	19.4	146	1	ANGI_SAGE
29	117.5	19.4	128	1	RNP_HORSE
30	116.5	19.2	124	1	RNP_CAMDR
31	116.5	19.2	128	1	RNP_PROGU
32	115.5	19.0	119	1	RNS4_BOVIN
33	115.5	19.0	146	1	ANGI_MACWU

34	114	18.8	148	1	ANGI_BOVIN
35	113.5	18.7	124	1	RNP_RANTA
36	113.5	18.7	146	1	ANGI_PAPHA
37	113	18.6	147	1	ANGI_HUMAN
38	113	18.6	147	1	ANGI_PANTR
39	112.5	18.5	124	1	RNP_CAPCA
40	112.5	18.5	124	1	RNP_GIRCA
41	112.5	18.5	148	1	RNS4_MOUSE
42	112	18.5	125	1	ANGI_RABIT
43	111.5	18.4	130	1	RNP_CRILO
44	111.5	18.4	147	1	RNS4_RAT
45	111.5	18.4	149	1	RNP_ACOCA

## ALIGNMENTS

RESULT 1  
RNPO\_RANCA STANDARD; PRT; 133 AA.  
AC P11916; Q9PWR7;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ribonuclease, oocytes precursor (EC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SHL-C).  
GN RCR.  
OS Rana catesbeiana (Bull frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
OX NCBI\_TaxID=8400;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=98165825; PubMed=9497370;  
RA Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;  
RT "The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.  
RT Tissue distribution, cloning, purification, cytotoxicity, and active  
RT residues for RNase activity.";  
RL J. Biol. Chem. 273:6395-6401(1998).  
[2]  
RN SEQUENCE OF 23-133.  
RP TISSUE=Egg;  
RX MEDLINE=87299649; PubMed=3304421;  
RA Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,  
RA Takayanagi G., Hakomori S.;  
RT "Amino acid sequence of sialic acid binding lectin from frog (Rana  
Rana catesbeiana) eggs";  
RL Biochemistry 26:2189-2194(1987).  
[3]  
RP CHARACTERIZATION, AND SEQUENCE OF 81-101.  
RX MEDLINE=92220613; PubMed=1373237;  
RA Liao Y.-D.;  
RT "A pyrimidine-guanine sequence-specific ribonuclease from Rana  
Rana catesbeiana (bullfrog) oocytes.";  
RL Nucleic Acids Res. 20:1371-1377(1992).  
[4]  
RP CHARACTERIZATION.  
RX TISSUE=Egg;  
RA Nitta K., Oyama F., Oyama K., Sekiguchi K., Kawauchi H.,  
RA Takayanagi Y., Hakomori S., Titani K.;  
RT "Ribonuclease activity of sialic acid-binding lectin from Rana  
Rana catesbeiana eggs.";  
RL Glycobiology 3:37-45(1993).  
[5]  
RP STRUCTURE BY NMR OF 23-133.  
RX MEDLINE=98437383; PubMed=9761686;  
RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;  
RT "The solution structure of a cytotoxic ribonuclease from the oocytes  
of Rana catesbeiana (bullfrog).";  
RL J. Mol. Biol. 283:231-244(1998).  
CC -!- FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine

```
QY 34 CKQVNTFISSATVKAICTG----VINNVLSSTRFQNLNCTRTSITPR-PCPYSSRTE 88
DB 39 CKQVNTFIHGTRNDIKAKCNDKNGEPYNFRSRKSPFQITTCCHKGGSNRPPCGYRATAG 98
QY 89 TNYICKVCENQYPVHF 104
DB 99 FRTIACVACENGLPVHF 114

RESULT 15
NRGPB
pancreatic ribonuclease (EC 3.1.27.5) B - guinea pig (tentative sequence)
N;Alternate names: RNase IB
C;Species: Cavia porcellus (guinea pig)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Accession: A00826
R;van den Berg, A.; van den Hende-Timmer, L.; Hofsteenge, J.; Gaastra, W.; Beintema, J.J.
Eur. J. Biochem. 75, 91-100, 1977
A;Title: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structure a
A;Reference number: A91247; MUID: 77185023; PMID: 862624
A;Accession: A00826
A;Molecule type: protein
A;Residues: 1-128 <VAN>
A;Note: 64-Pro was also found
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;21,34/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

Query Match 19.5%; Score 118.5; DB 1; Length 128;
Best Local Similarity 31.6%; Pred. No. 8.5e-05;
Matches 37; Conservative 14; Mismatches 43; Indels 23; Gaps 6;

QY 7 FQOKHI-----INTPIICNTIMDNNIYVGQCKRVNTFISSATVKAICTGVINNV 60
DB 8 FQRQHMDEGSPSPSNVNCVNMIRR-NMTQGRCKPVNTFVHESLADVQAVC---FQKNV 63
QY 61 L-----STTRFQNLNCTRTSITPR-CPYSSRTEINYICKVCENQ--YPVHF 104
DB 64 LCKNGQTCYQYSRMRITDCRVTSKSPFNGSYRMSQAKSIIVACEGDPYPVHF 120

Search completed: May 7, 2004, 21:54:55
Job time : 10.072 secs
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Db 6 AKPERHIDNSPSSVSSNYCNQMKSR-NLTQGRCKPVNTFVHESLADVQAVCS---QK 61  
 QY 59 NVL-----STTRFQNLNCTRTSITPRP-CPYSSRTENYICVKCE-NOY-PVHF 104  
 Db 62 NVACKNGQNCYQSYSTMSITDCRETGSSKYPNCAYKTTQAKKHIIIVACEGPNYPVPHY 120

RESULT 11

NRKGR  
 A:Title: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of mouse pancreatic ribonuclease (EC 3.1.1.27.5) - red kangaroo  
 N:Alternate names: RNase 1; RNase A  
 C:Species: Macropus rufus, Megaleia rufa (red kangaroo)  
 C:Date: 30-Nov-1980 #sequence\_revision 30-Nov-1980 #text\_change 04-Oct-1996  
 C:Accession: A00833  
 R:Gaasstra, W.; Wellington, G.W.; Beintema, J.J.  
 Eur. J. Biochem. 86, 209-217, 1978  
 A:Title: The amino-acid sequence of kangaroo pancreatic ribonuclease.  
 A:Reference number: A00833; MUID:78190621; PMID:658039  
 A:Accession: A00833  
 A:Molecule type: protein  
 A:Residues: 1-122 <GAA>  
 C:Superfamily: pancreatic ribonuclease  
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
 F:11,40,117/Active site: His, Lys, His #status predicted  
 F:25-83,39-94,57-109,64-71/Disulfide bonds: #status predicted  
 F:61/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 20.1%; Score 122; DB 1; Length 122;  
 Best Local Similarity 30.7%; Pred. No. 3.6e-05;  
 Matches 35; Conservative 16; Mismatches 45; Indels 18; Gaps 6;  
 QY 7 FQQRH-----INTPIICNTIMNNIYVGGCKRVNTFISSATTVKATC----- 52  
 Db 7 FQQRHDEHSTASSNYCNLMKAR-DMTSGRCKPLNTFHEPKSVVDVACHGENTCK 65  
 QY 53 TGVNMMVLSITRQNLNCTRTSITPRP-CPYSSRTENYICVKCE-NOY-PVHF 104  
 Db 66 NGRINC-YKSNRLSITNCRQFGASKYPCQYETSLNKLIIIVACEGQYVPVHF 118

RESULT 12

NRKU  
 A:Title: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of mouse pancreatic ribonuclease (EC 3.1.1.27.5) - nutria (tentative sequence)  
 N:Alternate names: RNase 1; RNase A  
 C:Species: Myocastor coypus (nutria, coypu)  
 C:Date: 24-Apr-1984 #sequence\_revision 30-Sep-1988 #text\_change 31-Mar-2000  
 C:Accession: A00822  
 R:van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.  
 Biochim. Biophys. Acta 453, 400-409, 1976  
 A:Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic ribonuclease.  
 A:Reference number: A90612; MUID:77065676; PMID:999896  
 A:Accession: A00822  
 A:Molecule type: protein  
 A:Residues: 1-128 <VAN>  
 C:Superfamily: pancreatic ribonuclease  
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
 F:12,41,119/Active site: His, Lys, His #status predicted  
 F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted  
 F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 19.9%; Score 120.5; DB 1; Length 128;  
 Best Local Similarity 31.6%; Pred. No. 5.4e-05;  
 Matches 37; Conservative 15; Mismatches 42; Indels 23; Gaps 7;  
 QY 7 FQQRH-----INTPIICNTIMNNIYVGGCKRVNTFISSATTVKATC----- 60  
 Db 8 FQQRHDSRGSPTNPNYCNQMKSR-NMTQGRCKPVNTFVHESLADVQAVC---FQKNV 63  
 QY 61 L-----STTRFQNLNCTRTSITPRP-CPYSSRTENYICVKCE-NOY-PVHF 104  
 Db 64 LCKNGQNCYQSNMHIIDCRVTSNDSYPCQYETSLNKLIIIVACEGQYVPVHF 120

RESULT 13

NRMS  
 A:Title: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of mouse pancreatic ribonuclease (EC 3.1.1.27.5) precursor - mouse  
 N:Alternate names: RNase 1; RNase A  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Nov-1980 #sequence\_revision 13-Mar-1997 #text\_change 18-Jun-1999  
 C:Accession: A34090; S22598; A00830  
 R:Schueller, C.; Nijssen, H.M.J.; Kok, R.; Beintema, J.J.  
 Mol. Biol. Evol. 7, 29-44, 1990  
 A:Title: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of mouse pancreatic ribonuclease (EC 3.1.1.27.5) precursor - mouse  
 A:Reference number: A34090; MUID:90136034; PMID:2299980  
 A:Accession: A34090  
 A:Molecule type: mRNA  
 A:Residues: 1-149 <SCH>  
 A:Cross-references: GB:M27814; NID:G200762; PIDN:AAA40060.1; PID:G200763  
 R:Samuelson, L.C.; Wiebauer, K.; Howard, G.; Schmid, R.M.; Koeplin, D.; Meisler, M.H.  
 Nucleic Acids Res. 19, 6935-6941, 1991  
 A:Title: Isolation of the murine ribonuclease gene Rib-1: structure and tissue specific expression.  
 A:Reference number: S22598; MUID:92107684; PMID:1840677  
 A:Accession: S22598  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-149 <SAM>  
 A:Cross-references: EMBL:X60103; NID:G53981; PIDN:CAA42697.1; PID:G53982  
 R:Lenstra, J.A.; Beintema, J.J.  
 Eur. J. Biochem. 98, 399-408, 1979  
 A:Title: The amino acid sequence of mouse pancreatic ribonuclease.  
 A:Reference number: A00830; MUID:80024269; PMID:556267  
 A:Accession: A00830  
 A:Molecule type: protein  
 A:Residues: 26-149 <LEN>  
 C:Superfamily: pancreatic ribonuclease  
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
 F:1-25/Domain: signal sequence #status predicted <SIG>  
 F:26-149/Product: pancreatic ribonuclease #status experimental <MAT>  
 F:37,66,144/Active site: His, Lys, His #status predicted  
 F:51-109,65-120,83-135,90-97/Disulfide bonds: #status predicted  
 F:62,87/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.9%; Score 120.5; DB 1; Length 149;  
 Best Local Similarity 30.8%; Pred. No. 6.3e-05;  
 Matches 36; Conservative 16; Mismatches 42; Indels 23; Gaps 7;  
 QY 7 FQQRH-----INTPIICNTIMNNIYVGGCKRVNTFISSATTVKATC----- 60  
 Db 33 FQQRHMDPGSSINSPTYCNQMKRR-DMTGSKCPVNTFVHESLADVQAVCS---QENV 88  
 QY 61 L-----STTRFQNLNCTRTSITPRP-CPYSSRTENYICVKCE-NOY-PVHF 104  
 Db 89 TCKRKNCKYKSSSALHITDCHLKGSKYPNCDYKTYQKHIIIVACEGPNYPVHF 145

RESULT 14

A43825  
 A:Title: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of mouse pancreatic ribonuclease (EC 3.1.1.27.5) - domestic pig  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: S29834; A43825  
 R:Bond, M.D.; Strydom, D.J.; Vallee, B.L.  
 Biochim. Biophys. Acta 1162, 177-186, 1993  
 A:Title: Characterization and sequencing of rabbit, pig and mouse angiogenins: discernmer  
 A:Reference number: S29833; MUID:93192291; PMID:8448182  
 A:Accession: S29834  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-123 <BON>  
 A:Note: this sequence was submitted to the Protein Sequence Database, December 1992  
 C:Superfamily: pancreatic ribonuclease

Query Match 19.7%; Score 119.5; DB 1; Length 123;  
 Best Local Similarity 39.5%; Pred. No. 6.5e-05;  
 Matches 30; Conservative 6; Mismatches 35; Indels 5; Gaps 2;





N/Alternate names: RNase 1; RNase A  
C/Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)  
C/Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 03-Jun-1994  
C/Accession: A00818  
R/Emmons, M.; Welling, G.W.; Beintema, J.J.  
Biochem. J. 157, 317-323, 1976  
A/Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease.  
F:26-84,40-95,110,65-72/Disulfide bonds: #status predicted  
F:76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental  
A/Accession: A00818  
A/Molecule type: protein  
A/Residues: 1-124 <EMM>  
C/Superfamily: pancreatic ribonuclease  
C/Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
F:12,41,119/Active site: His, Lys, His #status predicted  
F:26-84,40-95,110,65-72/Disulfide bonds: #status predicted  
F:76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 22.3%; Score 135.5; DB 1; Length 124;  
Best Local Similarity 33.3%; Pred. No. 1.7e-06;  
Matches 39; Conservative 16; Mismatches 39; Indels 23; Gaps 7;

QY 7 FQKQKHII-----NTPICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINNNV 60  
DB 8 FQKQKHSNPNPNYCNQMMRR-KMTQGRCKPVNTFVHESLEDKAVCS---QKNV 63  
QY 61 L-----STRFQNLNCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 104  
DB 64 LCKNGRTNCVESNSTWHITDCRQTGSSKYPNCAYKTSQKEKHIIIVACEGPNYPVHF 120

Query Match 61.6%; Score 374; DB 2; Length 111;  
Best Local Similarity 65.8%; Pred. No. 2.8e-30;  
Matches 73; Conservative 9; Mismatches 27; Indels 2; Gaps 2;

QY 2 QNWATFOQKHIIINPPI-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVI-NMN 59  
DB 1 QNWAKFKKHIIINPPI-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVI-NMN 59  
QY 60 VLSTTRFQNLNCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFAGIGRC 110  
DB 61 VLSTTRFQNLNCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFAGIGRC 111

Query Match 45.2%; Score 274.5; DB 2; Length 104;  
Best Local Similarity 48.6%; Pred. No. 2.1e-20;  
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 2 QNWATFOQKHIIINPPI-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVI-NMN 59  
DB 1 EDWLTFOQKHIIINPPI-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVI-NMN 59  
QY 60 VLSTTRFQNLNCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFAGIGRC 110  
DB 57 VLTISFYLSDC---NVTSPCKYKLLKSTNKEFCVTCENQAPVHFGVGC 104

Query Match 45.2%; Score 274.5; DB 2; Length 104;  
Best Local Similarity 48.6%; Pred. No. 2.1e-20;  
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 2 QNWATFOQKHIIINPPI-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVI-NMN 59  
DB 1 EDWLTFOQKHIIINPPI-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVI-NMN 59  
QY 60 VLSTTRFQNLNCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFAGIGRC 110  
DB 57 VLTISFYLSDC---NVTSPCKYKLLKSTNKEFCVTCENQAPVHFGVGC 104

Query Match 45.2%; Score 274.5; DB 2; Length 104;  
Best Local Similarity 48.6%; Pred. No. 2.1e-20;  
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 2 QNWATFOQKHIIINPPI-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVI-NMN 59  
DB 1 EDWLTFOQKHIIINPPI-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVI-NMN 59  
QY 60 VLSTTRFQNLNCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFAGIGRC 110  
DB 57 VLTISFYLSDC---NVTSPCKYKLLKSTNKEFCVTCENQAPVHFGVGC 104

N/Alternate names: RNase 1; RNase A  
C/Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)  
C/Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 03-Jun-1994  
C/Accession: A00818  
R/Emmons, M.; Welling, G.W.; Beintema, J.J.  
Biochem. J. 157, 317-323, 1976  
A/Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease.  
F:26-84,40-95,110,65-72/Disulfide bonds: #status predicted  
F:76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental  
A/Accession: A00818  
A/Molecule type: protein  
A/Residues: 1-124 <EMM>  
C/Superfamily: pancreatic ribonuclease  
C/Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
F:12,41,119/Active site: His, Lys, His #status predicted  
F:26-84,40-95,110,65-72/Disulfide bonds: #status predicted  
F:76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 22.3%; Score 135.5; DB 1; Length 124;  
Best Local Similarity 33.3%; Pred. No. 1.7e-06;  
Matches 39; Conservative 16; Mismatches 39; Indels 23; Gaps 7;

QY 7 FQKQKHII-----NTPICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINNNV 60  
DB 8 FQKQKHSNPNPNYCNQMMRR-KMTQGRCKPVNTFVHESLEDKAVCS---QKNV 63  
QY 61 L-----STRFQNLNCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 104  
DB 64 LCKNGRTNCVESNSTWHITDCRQTGSSKYPNCAYKTSQKEKHIIIVACEGPNYPVHF 120

Query Match 61.6%; Score 374; DB 2; Length 111;  
Best Local Similarity 65.8%; Pred. No. 2.8e-30;  
Matches 73; Conservative 9; Mismatches 27; Indels 2; Gaps 2;

QY 2 QNWATFOQKHIIINPPI-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVI-NMN 59  
DB 1 QNWAKFKKHIIINPPI-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVI-NMN 59  
QY 60 VLSTTRFQNLNCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFAGIGRC 110  
DB 61 VLSTTRFQNLNCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFAGIGRC 111

Query Match 45.2%; Score 274.5; DB 2; Length 104;  
Best Local Similarity 48.6%; Pred. No. 2.1e-20;  
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 2 QNWATFOQKHIIINPPI-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVI-NMN 59  
DB 1 EDWLTFOQKHIIINPPI-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVI-NMN 59  
QY 60 VLSTTRFQNLNCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFAGIGRC 110  
DB 57 VLTISFYLSDC---NVTSPCKYKLLKSTNKEFCVTCENQAPVHFGVGC 104

Query Match 45.2%; Score 274.5; DB 2; Length 104;  
Best Local Similarity 48.6%; Pred. No. 2.1e-20;  
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 2 QNWATFOQKHIIINPPI-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVI-NMN 59  
DB 1 EDWLTFOQKHIIINPPI-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVI-NMN 59  
QY 60 VLSTTRFQNLNCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFAGIGRC 110  
DB 57 VLTISFYLSDC---NVTSPCKYKLLKSTNKEFCVTCENQAPVHFGVGC 104

Query Match 45.2%; Score 274.5; DB 2; Length 104;  
Best Local Similarity 48.6%; Pred. No. 2.1e-20;  
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 2 QNWATFOQKHIIINPPI-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVI-NMN 59  
DB 1 EDWLTFOQKHIIINPPI-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVI-NMN 59  
QY 60 VLSTTRFQNLNCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFAGIGRC 110  
DB 57 VLTISFYLSDC---NVTSPCKYKLLKSTNKEFCVTCENQAPVHFGVGC 104

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:38:36 ; Search time 10.072 Seconds  
(without alignments)  
1060.090 Million cell updates/sec

Title: US-09-961-400-17  
Perfect score: 607  
Sequence: 1 MQNWATFOQKHINTPIICN.....ICVKCENQYPVHFAGIGRCP 111  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*\*

1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	588.5	97.0	111	2	A27121
2	455	75.0	111	1	JX0120
3	374	61.6	111	2	JX0085
4	274.5	45.2	104	2	A39035
5	135.5	22.3	124	1	NRWHK
6	135.5	22.3	145	1	A35932
7	133.5	22.0	167	2	S20066
8	132.5	21.8	124	1	NRPG
9	131.5	21.7	119	2	S41111
10	122.5	20.2	124	1	NRPRH
11	122	20.1	122	1	NRKGR
12	120.5	19.9	128	1	NRGU
13	120.5	19.9	149	1	NRMS
14	119.5	19.7	123	1	A43825
15	118.5	19.5	128	1	NRGPB
16	117.5	19.4	128	1	NRHO
17	116.5	19.2	124	1	NRGM
18	116.5	19.2	124	1	NRMM
19	116.5	19.2	124	1	NRMB
20	116.5	19.2	128	1	NRKS
21	114.5	18.9	124	2	S08549
22	114	18.8	125	1	NRHUG
23	113.5	18.7	124	1	NRDEN
24	113	18.6	147	1	NRHUG
25	112.5	18.5	124	1	NRGF
26	112.5	18.5	124	1	NRDEO
27	112	18.5	125	1	B43825
28	111.5	18.4	130	2	S22808
29	110.5	18.2	124	1	NRBOB

30 110.5 18.2 124 1 NRWB pancreatic ribonuc  
31 110.5 18.2 124 1 NREKN pancreatic ribonuc  
32 110.5 18.2 124 2 S07141 pancreatic ribonuc  
33 110.5 18.2 150 1 NRBO pancreatic ribonuc  
34 110.5 18.2 158 2 I61900 eosinophil-derived  
35 109.5 18.0 124 1 NRSH pancreatic ribonuc  
36 108.5 17.9 119 2 JX0115 pancreatic ribonuc  
37 108.5 17.9 124 1 NRCB pancreatic ribonuc  
38 108.5 17.9 152 1 NRRT pancreatic ribonuc  
39 106.5 17.5 124 1 NRHP pancreatic ribonuc  
40 106.5 17.5 125 4 A47498 seminal ribonuclea  
41 106.5 17.5 150 1 NRBO5 pancreatic ribonuc  
42 104.5 17.2 124 1 NRGN pancreatic ribonuc  
43 104.5 17.2 125 2 S04503 pancreatic ribonuc  
44 104 17.1 125 2 S04503 pancreatic ribonuc  
45 103.5 17.1 124 2 S08546 pancreatic ribonuc

## ALIGNMENTS

## RESULT 1

A27121  
ribonuclease-related sialic acid-binding lectin - bullfrog  
C:Species: Rana catesbeiana (bullfrog)  
C>Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 30-Jun-1993  
C:Accession: A27121  
R;Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawauchi, H.; Takayanagi  
A;Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)  
A;Reference number: A27121; MUID:87299649; PMID:3304421  
A;Accession: A27121  
A;Molecule type: protein  
A;Residues: 1-111 <TIT>  
C:Superfamily: pancreatic ribonuclease  
C;Keywords: lectin

Query Match 97.0%; Score 588.5; DB 2; Length 111;  
Best Local Similarity 98.2%; Pred. No. 1.3e-51;  
Matches 109; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 2 QNWATFOQKHINTPII-CNTIMDNNIYVGGCKRVNTFISSATVKAICTGVINMV 60  
DB 1 ENWATFOQKHINTPII-CNTIMDNNIYVGGCKRVNTFISSATVKAICTGVINMV 60  
QY 61 LSTTRFQMLTCTRTSITPRCPYSKRTETNYICVKCENQYPVHFAGIGRCP 111  
DB 61 LSTTRFQMLTCTRTSITPRCPYSKRTETNYICVKCENQYPVHFAGIGRCP 111

## RESULT 2

JX0120  
ribonuclease-related sialic acid-binding lectin - Japanese frog  
C:Species: Rana japonica (Japanese frog)  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: JX0120  
R;Kamiya, I.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawauchi, H.; Takayanagi,  
J. Biochem. 108, 139-143, 1990  
A;Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.  
A;Reference number: JX0120; MUID:91035319; PMID:2229005  
A;Accession: JX0120  
A;Molecule type: protein  
A;Residues: 1-111 <KAM>  
A;Experimental source: egg  
C:Superfamily: pancreatic ribonuclease  
C;Keywords: lectin; pyroglutamic acid  
F;1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental  
F;19-72,34-82,52-97,94-111/Disulfide bonds: #status experimental

Query Match 75.0%; Score 455; DB 1; Length 111;  
Best Local Similarity 78.4%; Pred. No. 2.5e-38;  
Matches 87; Conservative 7; Mismatches 15; Indels 2; Gaps 2;

Search completed: May 7, 2004, 21:51:58  
Job time : 36.6155 secs

GENERAL INFORMATION:  
; APPLICANT: RYBAK, SUSANNA M.  
; APPLICANT: GOLDENBERG, DAVID M.  
; APPLICANT: NEWTON, DIANNE L.  
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
; FILE REFERENCE: 018733/1059  
; CURRENT APPLICATION NUMBER: US/09/961,400  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 60/079,751  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Rana catesbeiana  
US-09-961-400-24

Query Match 98.4%; Score 597; DB 10; Length 110;  
Best Local Similarity 100.0%; Pred. No. 3.1e-60;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NWATFQOKHIINTPIICNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVINMNVLS 62  
Db 2 NWATFQOKHIINTPIICNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVINMNVLS 61

QY 63 TTRFQOLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111  
Db 62 TTRFQOLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 13  
US-09-961-400-19  
; Sequence 19, Application US/09961400  
; Publication No. US20030124131A1  
; GENERAL INFORMATION:  
; APPLICANT: RYBAK, SUSANNA M.  
; APPLICANT: GOLDENBERG, DAVID M.  
; APPLICANT: NEWTON, DIANNE L.  
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT  
; FILE REFERENCE: 018733/1059  
; CURRENT APPLICATION NUMBER: US/09/961,400  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 60/079,751  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Rana catesbeiana  
US-09-961-400-19

Query Match 98.2%; Score 596; DB 10; Length 110;  
Best Local Similarity 98.2%; Pred. No. 4e-60;  
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QNWATFQOKHIINTPIICNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVINMNVL 61  
1 QNWATFQOKHIINTPIICNTILDNIIYVGQCKRVNTFISSATTVKAICTGVINLNL 60

52 STTRFQOLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111  
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Db 61 STTRFQOLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 14  
US-09-948-391A-19  
; Sequence 19, Application US/09948391A  
; Publication No. US20030027311A1  
; GENERAL INFORMATION:  
; APPLICANT: RYBAK, SUSANNA M.  
; APPLICANT: NEWTON, DIANNE L.  
; APPLICANT: The United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase  
; FILE REFERENCE: 015280-343110US  
; CURRENT APPLICATION NUMBER: US/09/948,391A  
; CURRENT FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: US 60/079,751  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: US 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Rana  
; OTHER INFORMATION: catesbeiana ribonuclease with Met22Leu and  
; OTHER INFORMATION: Met57Leu substitutions (recombinant RacORI  
; OTHER INFORMATION: Met22Leu Met57Leu)  
US-09-948-391A-19

Query Match 97.2%; Score 590; DB 10; Length 110;  
Best Local Similarity 97.3%; Pred. No. 2e-59;  
Matches 107; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QNWATFQOKHIINTPIICNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVINMNVL 61  
Db 1 QNWATFQOKHIINTPIICNTILDNIIYVGQCKRVNTFISSATTVKAICTGVINLNL 60

QY 62 STTRFQOLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111  
Db 61 STTRFQOLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 15  
US-09-948-391A-6  
; Sequence 6, Application US/09948391A  
; Publication No. US20030027311A1  
; GENERAL INFORMATION:  
; APPLICANT: RYBAK, SUSANNA M.  
; APPLICANT: NEWTON, DIANNE L.  
; APPLICANT: The United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase  
; FILE REFERENCE: 015280-343110US  
; CURRENT APPLICATION NUMBER: US/09/948,391A  
; CURRENT FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: US 60/079,751  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: US 09/622,613  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 105